

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2004, 00:22:53 ; Search time 10175.3 Seconds  
(without alignments)  
12622.391 Million cell updates/sec

Title: US-09-931-157-2  
Perfect score: 4301  
Sequence: 1 gagacattccggtgggggac.....ctgggaaaaaaaaaaaaaa 4301

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_mam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result | Query |        |       |        |             | Description        |
|--------|-------|--------|-------|--------|-------------|--------------------|
|        | No.   | Score  | Match | Length | ID          |                    |
|        | 1     | 1372.2 | 31.9  | 3878   | 11 AK083415 | AK083415 Mus muscu |
|        | 2     | 1371.2 | 31.9  | 3990   | 11 AK085532 | AK085532 Mus muscu |
|        | 3     | 1329   | 30.9  | 1329   | 29 AY415512 | AY415512 Homo sapi |
|        | 4     | 1137.6 | 26.4  | 2521   | 11 AK082103 | AK082103 Mus muscu |
|        | 5     | 1126.4 | 26.2  | 3611   | 11 AK085165 | AK085165 Mus muscu |
|        | 6     | 1020   | 23.7  | 2669   | 11 AK076426 | AK076426 Mus muscu |
|        | 7     | 996    | 23.2  | 1329   | 29 AY415514 | AY415514 Mus muscu |
| c      | 8     | 987    | 22.9  | 1201   | 9 AL571798  | AL571798 AL571798  |
|        | 9     | 936.6  | 21.8  | 1144   | 29 AY415513 | AY415513 Pan trogl |
| c      | 10    | 866    | 20.1  | 957    | 12 BI520706 | BI520706 603071813 |
| c      | 11    | 860.2  | 20.0  | 1201   | 9 AL553041  | AL553041 AL553041  |
|        | 12    | 851    | 19.8  | 942    | 9 AL543805  | AL543805 AL543805  |
|        | 13    | 848    | 19.7  | 891    | 13 BQ229233 | BQ229233 AGENCOURT |
|        | 14    | 816.2  | 19.0  | 1201   | 9 AL546465  | AL546465 AL546465  |
|        | 15    | 808.6  | 18.8  | 972    | 12 BI858627 | BI858627 603389094 |
| c      | 16    | 802.4  | 18.7  | 942    | 9 AL570142  | AL570142 AL570142  |
|        | 17    | 794.8  | 18.5  | 884    | 13 BU557315 | BU557315 AGENCOURT |
|        | 18    | 792    | 18.4  | 911    | 13 BQ719386 | BQ719386 AGENCOURT |
| c      | 19    | 788    | 18.3  | 1201   | 9 AL571072  | AL571072 AL571072  |
|        | 20    | 773.6  | 18.0  | 852    | 13 BU172663 | BU172663 AGENCOURT |
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|        | 23    | 741.8  | 17.2  | 770    | 12 BM014035 | BM014035 603639686 |
| c      | 24    | 740.2  | 17.2  | 942    | 13 BX345882 | BX345882 BX345882  |
|        | 25    | 738    | 17.2  | 999    | 13 BX417121 | BX417121 BX417121  |
|        | 26    | 736    | 17.1  | 1201   | 9 AL545283  | AL545283 AL545283  |
|        | 27    | 734.2  | 17.1  | 978    | 13 BQ683643 | BQ683643 AGENCOURT |
|        | 28    | 732.8  | 17.0  | 1121   | 12 BM926545 | BM926545 AGENCOURT |
|        | 29    | 729.2  | 17.0  | 758    | 12 BM014042 | BM014042 603639695 |
|        | 30    | 727.8  | 16.9  | 885    | 12 BG769122 | BG769122 602743382 |
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| c      | 34    | 706.2  | 16.4  | 800    | 9 AI760041  | AI760041 wg57e06.x |
|        | 35    | 705    | 16.4  | 716    | 9 AL699988  | AL699988 DKFZp686K |
| c      | 36    | 703    | 16.3  | 722    | 12 BM970305 | BM970305 UI-CF-EC1 |
| c      | 37    | 698.8  | 16.2  | 726    | 9 AI422064  | AI422064 tf57c12.x |
| c      | 38    | 697.4  | 16.2  | 866    | 9 AI188458  | AI188458 qd14d01.x |
|        | 39    | 696.8  | 16.2  | 771    | 9 AU116904  | AU116904 AU116904  |
|        | 40    | 691.4  | 16.1  | 934    | 13 BQ718019 | BQ718019 AGENCOURT |
|        | 41    | 686.4  | 16.0  | 839    | 9 AU136164  | AU136164 AU136164  |
| c      | 42    | 679.4  | 15.8  | 771    | 9 AI567763  | AI567763 tr62c07.x |
| c      | 43    | 673    | 15.6  | 699    | 12 BM974913 | BM974913 UI-CF-EC1 |
| c      | 44    | 662.6  | 15.4  | 751    | 9 AA651686  | AA651686 nn47b02.r |
|        | 45    | 661.6  | 15.4  | 941    | 13 BX345883 | BX345883 BX345883  |

## ALIGNMENTS

## RESULT 1

AK083415

LOCUS AK083415 3878 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030003K13 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK083415

VERSION AK083415.1 GI:26350536

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

## REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

## REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

## REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I &amp; II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

## REFERENCE 6

(bases 1 to 3878)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cdNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .3878 /organism="Mus musculus" /mol\_type="mRNA" /strain="C57BL/6J" /db\_xref="FANTOM\_DB:D030003K13" /db\_xref="MGI:2418502" /db\_xref="taxon:10090" /clone="D030003K13" /tissue\_type="whole body" /clone\_lib="RIKEN full-length enriched mouse cDNA library" /dev\_stage="9 days embryo"

CDS 109. .1437 /note="unnamed protein product; ENDOTHELIN B RECEPTOR PRECURSOR (SWISSPROT|P48302, evidence: FASTY, 100%ID, 100%length, match=1326) putative" /codon\_start=1 /protein\_id="BAC38908.1" /db\_xref="GI:26350537" /translation="MQSPASRCGRALVALLACGFLGVWGEKRGFPFPAQATLSLLGTK EVMTPTPTKTSWTRGSNSSLMRSSAPAEVTKGGRGAGVPPRSFPPPCQRNIEISKTFKY INTIVSCLVFVLGIIGNSTLLRIIYKNKCMRNGPNILIASLALGDLHLHIIDIPINTY KLLAEDWPFGAEMCKLVPFIQKASVGITVLSLCALSIDRYRAVASWSRIKIGVPKWT AVEIVLIWVSVVLAVPEAIGFDMITSYK GKPLRVCMLNPFQKTAFMQFYKTAKDWW LFSFYFCLPLAITAVFYTLMTCEMLRKSGMQIALNDHLKQRREVAKTVFCLVLVFAI CWLPLHLSRIKLTLTDQSNPHRCCELLSFLVLVDYIGINMASLNSCINPIALYLVSKR FKNCFKSCLCCWCQTFEKQSLKFKANDHGYDNFRSSNKKYSSS"

polyA\_signal 3859. .3864



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polyA_site                    3878
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ORIGIN

Query Match          31.9%;  Score 1372.2;  DB 11;  Length 3878;
Best Local Similarity 66.0%;  Pred. No. 8.1e-254;
Matches 2665;  Conservative 0;  Mismatches 1043;  Indels 327;  Gaps 34;

Qy      193  AAAGTGGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCTCCA 252
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Db      64  AAACAGCAGAGCGGCTACCAGACTCTCACAGGAGCAAGCTGTAACATGCAATCGCCCGCA 123

Qy      253  AGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCCTGTCGCGGATCTGG 312
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Db      124  AGCCGGTGGGACGCGCCTTGGTGGCGCTGCTGCTGGCCTGTGGCTTCTTGGGGGTATGG 183

Qy      313  GGAGAGGAGAGAGGCTTCCCGCCTGCAGGGCCACTC---CGCTTTTGCAAACCGCAGAG 369
          ||||| | | |||| | |||| |||| | | |||| | | | ||| | |||
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Qy      370  ATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGG 429
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Qy      430  TCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACC 489
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Db      304  TCCTCCGCACCTGCGGAGGTGACCAAAGGAGGGAGGGGGGCTGGAGTCCCGCCAAGATC- 362

Qy      490  ATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAAC 549
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Qy      550  ACGGTTGTGTCTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGA 609
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Db      421  ACGATTGTGTCTCTGCCTCGTGTTCGTGCTAGGCATCATCGGGAACCTCCACGCTGCTAAGA 480

Qy      610  ATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCT 669
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Db      481  ATCATCTACAAGAACAAGTGCATGCGCAATGGTCCCAATATCTTGATCGCCAGTCTGGCT 540

Qy      670  CTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCA 729
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Qy      730  GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC 789
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Qy      790  GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849
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Qy      850  TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAATGGACAGCAGTAGAAATTGTTTTG 909
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Qy 910 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969  
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 Db 781 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCGAAGCCATAGGTTTTGATATGATTACG 840

Qy 970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT 1029  
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 Db 841 TCGGACTACAAAGGAAAGCCCTAAGGGTCTGCATGCTTAATCCCTTTCAGAAAACAGCC 900

Qy 1030 TTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTG 1089  
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Qy 1150 AGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACC 1209  
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Qy 1270 CTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTG 1329  
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Qy 1330 TTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATT 1389  
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Qy 1390 GCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGCTGG 1449  
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Qy 1510 GCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG 1569  
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Qy 1570 AAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAAACAAAATG 1629  
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Qy 1630 AAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTATTAATAATAT 1689  
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Qy 1690 AAGTGTAATTATTTTAACTCAGCTACATATGAC-----ATTTTATGAGCTGTTTAC 1744  
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 Db 1561 AGAGGGATTATTTTAACTGTTCTGACGCTCAACACCGGATATATTCACGGGCTGTTTAC 1620

Qy 1745 GGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAATTTTT 1804

|    |      |  |      |
|----|------|--|------|
| Db | 1621 | AACCTAAGAAAGCTGTGGGAAGGAATGAAGCCCTCCTCCGTGGGGAAGCACTTAGATTCT   | 1680 |
| Qy | 1805 | TACAGTTAGCACTTCAACATAGCTCTTAACAACCTTCCAGGATATTCACACAACACTTAGG  | 1864 |
| Db | 1681 | T--AGTCAGCACTTCAGCAGAGCTCTTAAAGCCCCTAGTGCGTTCACATGCCACTTACG    | 1738 |
| Qy | 1865 | CTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTAAATC   | 1924 |
| Db | 1739 | TTTAAAAA-----AACGAGAACTTCACTGAAGTTCTGTTCAGGAGTTTATTATCCAGT     | 1791 |
| Qy | 1925 | AATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATGAAGC    | 1984 |
| Db | 1792 | CCTATGAATCTGGATTCAAGAAAGCAT--GACATTGCAAAACAATTCTTAAACGAAGTT    | 1849 |
| Qy | 1985 | TTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAACAACCTTTTCAATTAATATTATC | 2044 |
| Db | 1850 | TCAATTGCTTAATTTGAAACTTAAAAAAAAAAAACTAATAAATTTTTATGCATACTATC    | 1909 |
| Qy | 2045 | --ACACTATTATCAGATTGTAATTAGATGCAAAAGAGAGAGCAGTTTAGTTGTTGCA--TT  | 2101 |
| Db | 1910 | ATACCCACTAATCTGATTGTAACATATATGCAAAAGAAAAGGCAATATGGTTGGTAAACTT  | 1969 |
| Qy | 2102 | TTTCGGACACTGGAACATTTAAATGATCAGGAGGGAGTAACAGAAAAGCAAGGCTGTT     | 2161 |
| Db | 1970 | TTTTGGTCATTACCAACATGAAATGATCAGAATTCTGGGGGAAGAAA-----           | 2016 |
| Qy | 2162 | TTTGAAAATCATTACACTTTCACTAGAAAGCCCAAACCTCAGCATTTCTGCAATATGTAACC | 2221 |
| Db | 2017 | -----AGACAGCC  | 2024 |
| Qy | 2222 | AACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAT     | 2281 |
| Db | 2025 | TGCGAATGCCACAGAGAAAACATGGGAAAGCGTG-----                        | 2058 |
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| Db | 2059 | -----AGCTGCTATGCCTGAGACTTCTGAAATTCCTCACACATACTCTGCAG           | 2106 |
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| Db | 2107 | AAAGACACAAA-----ACAGAACACTACCTATGATTTCTTTAAAGTTCTTTCAAAT       | 2157 |
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| Db | 2158 | ATCCTTTCATGATTGAAGTTTAAATCCATGTGTTCAACTTCATCA-----             | 2203 |
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| Db | 2204 | -----TCTGTAAATACTTAGCTATTAGCTATAAGCAC                          | 2235 |
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| Db | 2236 | TACACGTAGAGGACTTAACAAAGGGCAGGTCCAGCGTTCGTAGCTTTCTGACAAAGAGA    | 2295 |
| Qy | 2580 | TGCCAGTGACCTCATAAT--AAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAA   | 2637 |

|    |      |   |      |
|----|------|---|------|
| Db | 2296 | TGCCAGTAACCCGGTTATAGACAGAATGTGAATTGCCCCGTGCAGTGTCCACATGGCAAA    | 2355 |
| Qy | 2638 | GGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTAT   | 2697 |
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| Qy | 2698 | AATGCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGT-ACATTTAACAGCTA    | 2756 |
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| Qy | 2757 | CCTGTAAAGCTTATTACTAA-TTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTT    | 2815 |
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| Db | 2468 | TCTCGGAGGCATACTACCAACTTTTTTATGTTATTCCTGAAAATAGCCAATAGAAAGGCGT   | 2527 |
| Qy | 2816 | GCTTGACATGGTGCTTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAAC    | 2875 |
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| Db | 2588 | CTCCT--CTTTGCGCATTCCTTGTCTAGGTTTTTTTTTTTTTTTTTTTAAATCTCCTTCCACG | 2645 |
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| Db | 2706 | AGAGAGAGGAAATGAGGTGGGGCCAGAGGAAGCCCGTGGGGAAATATCCCATTCTTAGC     | 2765 |
| Qy | 3042 | CTAACGTTTCGTCATTGCCTCGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAA     | 3101 |
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| Db | 2766 | CCTGTGTTTCGTCAC TGCCACGTCATGTCGGTGTGAAAGGTCCTGGTTCGGCTCCAGCAAA  | 2825 |
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| Db | 2826 | ACAAAGCGCAGCGTTCTCAGCGTGAC-TCGGGAACAAACCAAGCCCGAGAGCTTTAACCT    | 2884 |
| Qy | 3162 | GGTCTTAAAATATGCCCAAATTTT-----                                   | 3185 |
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| Db | 2885 | TGTCTTAAAATATAACAGATTTTCCTTCCTTCCTTTTTCTCTTCTTCTCTTCTCTC        | 2944 |
| Qy | 3186 | -----TACTTTGTTTTTCTTTTAATAGGCTGGGCCACATG                        | 3220 |
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| Qy | 3281 | AAAACCCAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTACACACCCATATGG    | 3340 |
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| Db | 3065 | CAAACGGGACAATGAGGTAAAAAACCAAGAACAATACTGAATCCACGTGACAC----ATG    | 3120 |
| Qy | 3341 | ATTCTATTTATAAATCACCCACAAACTTGTTCCTTTAATTTTCATCCCAATCACTTTTTCAG  | 3400 |
|    |      |   |      |
| Db | 3121 | ACTCTCTTTAGGAGTCACCCACAGTTCTTGTGTGTA-----CAGAT                  | 3161 |



DEFINITION Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630038G12 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK085532

VERSION AK085532.1 GI:26351656

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

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AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3990)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,

Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,  
 Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,  
 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
 Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission  
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)  
 COMMENT cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:http://genome.gsc.riken.go.jp/  
 URL:http://fantom.gsc.riken.go.jp/.  
 FEATURES Location/Qualifiers  
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# ORIGIN

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Qy 313 GGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTC---CGCTTTTGCAAACCGCAGAG 369  
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 Db 3514 ATATACAATAAACTATATTAAGTGGCTTTTTATTAAAAATTTAGCACA-----CAG 3567  
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 | | | | | ||| || | ||| | | ||| | | |||| |||| | |  
 Db 3568 ACCAAGGGTGATAAGAAAAAAACATGATCCCTTGCATAATTAACCAAGATAAGAGA 3627  
 Qy 3752 AGGTGCTATCGTTCAACTTCAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAAC 3811  
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 Db 3628 AGGTACCATCT---AATTTAAAGCATATTTTCTAACATTTAAGTAGCCTAATATAGCAAT 3684  
 Qy 3812 AGACAAAATTATTGTTAACATGGATGTTACAGCTCAAAGATTATATAAAGATTTTAACC 3871  
 | |||| | |||| || |||| || |||| |||| ||| || | | |  
 Db 3685 GCATAAAAATAGTGTTAACAAGGATGTTAGAGGTCAAACGATTTGTAAGTGACTTCAGCC 3744  
 Qy 3872 TATTTTCTCCCTTATTATCCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATT 3931  
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 Db 3745 TATTTTCTCCCAAATTATTTACTGCTATTTTGGTCTGTGTTCAAACA-TTTTCAGTATT 3803  
 Qy 3932 GATAGCTTACATATGGCCAAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCT 3991  
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 Db 3804 GATAATGTGCA-ACAGCCAAAGGAACACTGTTTTTCATCCAAATGCGGGTGTGTTGTACCT 3862  
 Qy 3992 AACTTTATAAAAGTGTAATATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGG 4051  
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 Db 3863 AAC---ATGCACTTGTAATAAAGCCGTGTAAAA---TAACTGTGTTTGTGTTTGCTCTGG 3916  
 Qy 4052 TTGCCTAAAGTGGC-----TATAGTTACTGATTTTTTTATTATGTAAGCAAACCAATAA 4105  
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 Db 3917 TCACCTAAAGTGGCAGCTTGTGTCGTTGCTAACTTCTTGTTGAGTAAGCAAACCAATAA 3976  
 Qy 4106 AAATTTAAGTTTTT 4119  
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 Db 3977 ACGTTCAAATGGTT 3990

# RESULT 3

AY415512

LOCUS AY415512 1329 bp DNA linear GSS 17-DEC-2003  
 DEFINITION Homo sapiens EDNRB gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 ACCESSION AY415512  
 VERSION AY415512.1 GI:39771471  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1329)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1329)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .1329

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

gene <1. .>1329

/gene="EDNRB"

/locus\_tag="HCM5582"

# ORIGIN

Query Match 30.9%; Score 1329; DB 29; Length 1329;

Best Local Similarity 100.0%; Pred. No. 2.2e-245;

Matches 1329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297

Db 1 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 60

Qy 298 CTGTGCGGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 357

Db 61 CTGTGCGGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 120

Qy 358 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 417

Db 121 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 180

Qy 418 AGTCTGGCGGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 477

Db 181 AGTCTGGCGGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 240

Qy 478 CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 537

Db 241 CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 300

Qy 538 AAATACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCC 597

Db 301 AAATACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCC 360

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| Qy | 598  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC | 657  |
|    |      |  |      |
| Db | 361  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC | 420  |
| Qy | 658  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC | 717  |
|    |      |  |      |
| Db | 421  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC | 480  |
| Qy | 718  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA | 777  |
|    |      |  |      |
| Db | 481  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA | 540  |
| Qy | 778  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT | 837  |
|    |      |  |      |
| Db | 541  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT | 600  |
| Qy | 838  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA | 897  |
|    |      |  |      |
| Db | 601  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA | 660  |
| Qy | 898  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT | 957  |
|    |      |  |      |
| Db | 661  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT | 720  |
| Qy | 958  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT | 1017 |
|    |      |  |      |
| Db | 721  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT | 780  |
| Qy | 1018 | CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAGTTTC | 1077 |
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| Db | 781  | CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAGTTTC | 840  |
| Qy | 1078 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATG | 1137 |
|    |      |  |      |
| Db | 841  | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATG | 900  |
| Qy | 1138 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA | 1197 |
|    |      |  |      |
| Db | 901  | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA | 960  |
| Qy | 1198 | GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC | 1257 |
|    |      |  |      |
| Db | 961  | GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC | 1020 |
| Qy | 1258 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT | 1317 |
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| Db | 1021 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT | 1080 |
| Qy | 1318 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC | 1377 |
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| Db | 1081 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC | 1140 |
| Qy | 1378 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGC  | 1437 |
|    |      |  |      |
| Db | 1141 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGC  | 1200 |

Qy 1438 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC 1497  
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 Db 1201 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC 1260  
 Qy 1498 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC 1557  
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 Db 1261 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC 1320  
 Qy 1558 TCATCTTGA 1566  
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 Db 1321 TCATCTTGA 1329

#### RESULT 4

AK082103

LOCUS AK082103 2521 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230007M01 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK082103

VERSION AK082103.1 GI:26349538

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

#### REFERENCE

1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

#### REFERENCE

2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

#### REFERENCE

3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

#### REFERENCE

4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2521)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.go.jp/  
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1..2521  
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# ORIGIN

Query Match 26.4%; Score 1137.6; DB 11; Length 2521;  
 Best Local Similarity 76.4%; Pred. No. 1.2e-208;  
 Matches 1507; Conservative 0; Mismatches 439; Indels 26; Gaps 8;

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| Qy | 193 | AAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCCA   | 252 |
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| Db | 168 | AAACAGCAGAGCGGCTACCAGACTCTCACAGGAGCAAGCTGTAACATGCAATCGCCCGCA  | 227 |
| Qy | 253 | AGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGGATCTGG  | 312 |
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| Db | 288 | GGAGAGAAAAGAGGATTCCACCTGCCAAGCCACGCTGTCACTTCTCGGGACTAAAGAG    | 347 |
| Qy | 370 | ATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGG  | 429 |
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| Db | 348 | GTAATGACGCCACCCACTAAGACCTCCTGGACCAGAGGTCCAACCTCAGTCTGATGCGT   | 407 |
| Qy | 430 | TCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACC  | 489 |
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| Db | 408 | TCCTCCGCACCTGCGGAGGTGACCAAAGGAGGGAGGGGGGCTGGAGTCCCGCCAAGATC-  | 466 |
| Qy | 490 | ATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAAC | 549 |
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| Qy | 550 | ACGGTTGTGTCTGCCTTGTGTTCTGCTGGGGATCATCGGGAACCCACACTTCTGAGA     | 609 |
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| Db | 585 | ATCATCTACAAGAACAAGTGCATGCGCAATGGTCCCAATATCTTGATCGCCAGTCTGGCT  | 644 |
| Qy | 670 | CTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCA  | 729 |
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| Db | 645 | CTGGGAGACCTACTGCACATCATATAGACATACCCATTAACACCTACAAGTTGCTCGCA   | 704 |
| Qy | 730 | GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC  | 789 |
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| Db | 705 | GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAGGCTTCT  | 764 |
| Qy | 790 | GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT  | 849 |
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| Db | 765 | GTGGGAATCACAGTGTGAGTCTTTGTGCTCTAAGTATTGACAGATATCGAGCTGTTGCT   | 824 |

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 Db 1725 AACCTAAGAAAGCTGTGGGAAGGAATGAAGCCCTCCTCCGTGGGGAAGCACTTAGATTCT 1784  
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 Qy 1865 CTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTAAATC 1924  
 Db 1843 TTTAAAAAACG-----AGAACTTCACTGAAGTTCTGTTCAGGAGTTTATTATCCAGT 1895  
 Qy 1925 AATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATGAAGC 1984  
 Db 1896 CCTATGAATCTGGATTCAAGAAAGCATGA---CATTGCAAAACAATTCTTAAACGAAGT 1952  
 Qy 1985 TTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACCTTTTCAATTAATATTATC 2044  
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 Db 2013 ATACCCACTAATCTGATTGTAACATATATGCAAAAGAAAAGGCAATATGGTTGGTAAACTT 2072  
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 Db 2073 TTTTGGTCATTACCAACATTGAAATGATCAGAATTCGGGGGAAGAAAAGACA 2124

# RESULT 5

AK085165

LOCUS AK085165 3611 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone:D430047G06 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK085165

VERSION AK085165.1 GI:26351484

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
 Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,  
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
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 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
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 MEDLINE 20530913  
 PUBMED 11076861  
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 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
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 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 3611)  
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
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 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
 Muramatsu,M. and Hayashizaki,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)  
 COMMENT cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:http://genome.gsc.riken.go.jp/  
 URL:http://fantom.gsc.riken.go.jp/.  
 FEATURES Location/Qualifiers  
 source 1. .3611

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# ORIGIN

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| Db | 1489 | AAGCCAACGATCACGGATATGACAACTTCCGGTCCAGCAATAAATACAGCTCGTCTTGAA  | 1548 |
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| Qy | 1743 | ACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAATTT   | 1802 |
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| Db | 1847 | CGTTTTAAAAA-----AACGAGAACTTCACTGAAGTTCTGTTTCAAGAGTTTATTATCCA  | 1899 |
| Qy | 1923 | TCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATGAA  | 1982 |
| Db | 1900 | GTCCTATGAATCTGGATTCAAGAAAGCAT--GACATTGCAAACAATTCTTAAACGAAG    | 1957 |
| Qy | 1983 | GCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATATTA | 2042 |
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| Db | 2018 | TCATACCCACTAATCTGATTGTAAGTATATGCAAAGAAAAGGCAATATGGTTGGTAAAC   | 2077 |
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| Db | 2078 | TTTTTTGGTCATTACCAACATTGAAATGATCAGAATTCGGGGGAAGAAAAGACAG----   | 2132 |
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| Db | 2133 | -----   | 2132 |
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| Db | 2133 | CCTGCGAATGCCACAGAGAAAACATGGGAAAGCGTG-----                     | 2168 |
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| Db | 2169 | -----AGCTGCTATGCCTGAGACTTCTGAAATTCCCTCACACATACTCTGC           | 2214 |
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| Qy | 2874 | ACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGG  | 2933 |
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| Db | 3392 | TTAATTTTACT-AAGTTTTAGATTGGTTTTATTGTTGTGTTCTAAATTCCTAAGTCCTA    | 3450 |
| Qy | 3546 | ATACCCTTTCCT-----TCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAA      | 3597 |
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ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636

REFERENCE 2  
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Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
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PUBMED 11042159

REFERENCE 3  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,  
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TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
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JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
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TITLE Functional annotation of a full-length mouse cDNA collection  
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Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
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Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.go.jp/  
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers  
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/mol\_type="mRNA"  
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/db\_xref="MGI:2391324"  
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#### ORIGIN

Query Match 23.7%; Score 1020; DB 11; Length 2669;  
Best Local Similarity 84.7%; Pred. No. 5.1e-186;  
Matches 1169; Conservative 0; Mismatches 205; Indels 6; Gaps 2;

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Db 235 AGCCGGTGC GGACGCGCCTTGGTGGCGCTGCTGCTGGCCTGTGGCTTCTTGGGGGTATGG 294  
Qy 313 GGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTC---CGCTTTTGCAAACCGCAGAG 369  
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Db 295 GGAGAGAAAAGAGGATTCCACCTGCCCAAGCCACGCTGTCACTTCTCGGGACTAAAGAG 354  
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| Qy | 1210 | GTCTTTTGCCTGGTCTCTTGCTTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATT | 1269 |
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| Qy | 1270 | CTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTG  | 1329 |
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| Qy | 1330 | TTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCCTGCATTAACCCAATT | 1389 |
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| Qy | 1390 | GCTCTGTATTTGGTGAGCAAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGG  | 1449 |
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| Qy | 1450 | TGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAA   | 1509 |
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| Db | 1432 | TGCCAAACGTTTGAGGAAAAGCAGTCCTTGGAGGAGAAGCAGTCCTGCCTGAAGTTCAA   | 1491 |
| Qy | 1510 | GCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG  | 1569 |
|    |      |   |      |
| Db | 1492 | GCCAAACGATCACGGATATGACAACTTCCGGTCCAGCAATAAATACAGCTCGTCTTGAAGG | 1551 |

AY415514

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| LOCUS | AY415514 | 1329 bp | DNA | linear | GSS 17-DEC-2003 |
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DEFINITION Mus musculus EDNRB gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY415514

VERSION AY415514.1 GI:39771473

KEYWORDS GSS.

SOURCE *Mus musculus* (house mouse)

|          |              |
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| ORGANISM | Mus musculus |
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1329)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

|       |  |
|-------|--|
| TITLE | Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios |
|-------|--|

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1329)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

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FEATURES                      Location/Qualifiers
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Best Local Similarity 85.3%;  Pred. No. 2.5e-181;
Matches 1136;  Conservative 0;  Mismatches 190;  Indels 6;  Gaps 2;

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Qy      355 TTGCAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAAC 414
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Qy      415 GCCAGTCTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGA 474
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 Db 898 ATGCTCAGGAAGAAGAGCGGTATGCAGATTGCTTTGAATGATCACTTAAAGCAGAGACGA 957  
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 Db 1318 AGCTCGTCTTGA 1329

RESULT 8

AL571798/c

LOCUS AL571798 1201 bp mRNA linear EST 31-MAY-2003

DEFINITION AL571798 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 clone CS0DI030YM19 3-PRIME, mRNA sequence.

ACCESSION AL571798

VERSION AL571798.2 GI:31293189

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| KEYWORDS  | EST.   |
| SOURCE    | Homo sapiens (human)   |
| ORGANISM  | Homo sapiens<br>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  |
| REFERENCE | 1 (bases 1 to 1201)  |
| AUTHORS   | Li,W.B., Gruber,C., Jessee,J. and Polayes,D.   |
| TITLE     | Full-length cDNA libraries and normalization   |
| JOURNAL   | Unpublished (2001)   |
| COMMENT   | On Feb 16, 2001 this sequence version replaced gi:12929453.<br>Contact: Genoscope<br>Genoscope - Centre National de Sequencage<br>BP 191 91006 EVRY cedex - France<br>Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr<br>Library was constructed by Life Technologies, a division of<br>Invitrogen. This sequence belongs to sequence cluster 7006.r For<br>more information about this cluster, see<br><a href="http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI030AG10NP1&amp;cluster=7006.r">http://www.genoscope.cns.fr/<br/>cgi-bin/cluster.cgi?seq=CS0DI030AG10NP1&amp;cluster=7006.r</a> . Contact :<br>Feng Liang Email : <a href="mailto:fliang@lifetech.com">fliang@lifetech.com</a> URL :<br><a href="http://fulllength.invitrogen.com/">http://fulllength.invitrogen.com/</a> InVitroGen Corporation 1600<br>Faraday Avenue Genoscope sequence ID : CS0DI030AG10NP1. |

ORIGIN

Query Match 22.9%; Score 987; DB 9; Length 1201;  
Best Local Similarity 96.0%; Pred. No. 1.4e-179;  
Matches 1030; Conservative 10; Mismatches 28; Indels 5; Gaps 3;

[illegible]



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| Qy | 789  | CGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGC       | 848  |
| Db | 773  | <br>CGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGC   | 714  |
| Qy | 849  | TTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAAATTGTTTT      | 908  |
| Db | 713  | <br>TTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAAATTGTTTT  | 654  |
| Qy | 909  | GATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTAC       | 968  |
| Db | 653  | <br>GATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTAC   | 594  |
| Qy | 969  | GATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGC       | 1028 |
| Db | 593  | <br>GATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGC   | 534  |
| Qy | 1029 | TTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTT     | 1088 |
| Db | 533  | <br>TTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTT | 474  |
| Qy | 1089 | GCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAA      | 1148 |
| Db | 473  | <br>GCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAA  | 414  |
| Qy | 1149 | AAGTGGCATGCAGATTGCTTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAAC      | 1208 |
| Db | 413  | <br>AAGTGGCATGCAGATTGCTTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAAC  | 354  |
| Qy | 1209 | CGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTCAGCAGGAT        | 1268 |
| Db | 353  | <br>CGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTCAGCAGGAT    | 294  |
| Qy | 1269 | TCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCT       | 1328 |
| Db | 293  | <br>TCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCT   | 234  |
| Qy | 1329 | GTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAAT       | 1388 |
| Db | 233  | <br>GTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAAT   | 174  |
| Qy | 1389 | TGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTG        | 1448 |
| Db | 173  | <br>TGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTG    | 114  |
| Qy | 1449 | GTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAA       | 1508 |
| Db | 113  | <br>GTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAA   | 54   |
| Qy | 1509 | AGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCAT               | 1561 |
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AY415513  
 LOCUS AY415513 1144 bp DNA linear GSS 17-DEC-2003  
 DEFINITION Pan troglodytes EDNRB gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 ACCESSION AY415513  
 VERSION AY415513.1 GI:39771472  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 REFERENCE 1 (bases 1 to 1144)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 1144)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
 FEATURES Location/Qualifiers  
 source 1. .1144  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 gene <1. .>1144  
 /gene="EDNRB"  
 /locus\_tag="HCM5582"  
 ORIGIN

Query Match 21.8%; Score 936.6; DB 29; Length 1144;  
 Best Local Similarity 82.1%; Pred. No. 7e-170;  
 Matches 939; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

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Qy      423  GGC GCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCC 482
          |||
Db      1    GGC GCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCC 60

Qy      483  ACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATA 542
          |||
Db      61  ACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATA 120

Qy      543  CATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACT 602
          |||
Db      121  CATNNACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACT 180

Qy      603  TCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAG 662

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|    |      |   |      |
|----|------|---|------|
| Db | 181  | TCTGAGNNTTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAG      | 240  |
| Qy | 663  | CTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCT      | 722  |
| Db | 241  | CTTGGCTCTGGNNCT | 300  |
| Qy | 723  | GCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAA      | 782  |
| Db | 301  | GCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAA      | 360  |
| Qy | 783  | AGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGC      | 842  |
| Db | 361  | AGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGC      | 420  |
| Qy | 843  | TGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAAT      | 902  |
| Db | 421  | TGTTGCATCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAAT      | 480  |
| Qy | 903  | TGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATAT      | 962  |
| Db | 481  | TGTTTTGATTTGGGTGGTCTCTGTGGTTCTAGCTGTCCCTGAAGCCATAGGTTTTGATAT      | 540  |
| Qy | 963  | AATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAA      | 1022 |
| Db | 541  | AATTACGATGGACTACAAAGGAAGTTATCTACGAATCTGCTTGCTTCATCCCGTTCAGAA      | 600  |
| Qy | 1023 | GACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTGAGTTTCTATTT     | 1082 |
| Db | 601  | GACAGCTTTCATGCAGNN  | 660  |
| Qy | 1083 | CTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAG     | 1142 |
| Db | 661  | NN    | 720  |
| Qy | 1143 | AAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGC      | 1202 |
| Db | 721  | NN    | 780  |
| Qy | 1203 | CAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAG      | 1262 |
| Db | 781  | CAAAACTGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAG      | 840  |
| Qy | 1263 | CAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTGAG      | 1322 |
| Db | 841  | CAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTGAG      | 900  |
| Qy | 1323 | CTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAA      | 1382 |
| Db | 901  | CTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAA      | 960  |
| Qy | 1383 | CCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTATG        | 1442 |
| Db | 961  | CCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTATG        | 1020 |
| Qy | 1443 | CTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAA      | 1502 |

Db 1021 CTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAA 1080

Qy 1503 GTTCAAAGCTAATGATCACGGATATGACAACCTTCCGTTCCAGTAATAAATACAGCTCATC 1562  
 |||

Db 1081 GTTCAAAGCTAATGATCACGGATATGACAACCTTCCGTTCCAGTAATAAATACAGCTCATC 1140

Qy 1563 TTGA 1566  
 |||

Db 1141 TTGA 1144

RESULT 10

BI520706/c

LOCUS BI520706 957 bp mRNA linear EST 29-AUG-2001

DEFINITION 603071813T1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5163746 3',  
 mRNA sequence.

ACCESSION BI520706

VERSION BI520706.1 GI:15345498

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 957)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11406 row: j column: 03

High quality sequence start: 4

High quality sequence stop: 954.

FEATURES

source

Location/Qualifiers

1. .957

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5163746"

/tissue\_type="medulla"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_119"

/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: EcoRV (destroyed); RNA source normal medulla from  
 anonymous male age 27. Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.3 kb, insert size range  
 0.9-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 013. Note:  
 this is a NIH\_MGC Library."

ORIGIN

Query Match 20.1%; Score 866; DB 12; Length 957;  
 Best Local Similarity 96.5%; Pred. No. 2.8e-156;  
 Matches 917; Conservative 0; Mismatches 30; Indels 3; Gaps 3;

|    |      |  |      |
|----|------|--|------|
| Qy | 569  | TGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAACAAGT | 628  |
|    |      |  |      |
| Db | 956  | TGTTTCGTGCTGGGGATCATCCGGAACCTCCACACTTCTGAGAATACTCTACAGAACCAAGG | 897  |
| Qy | 629  | GCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACA   | 688  |
|    |      |  |      |
| Db | 896  | CAATGCGAAACGGTCCCAATATCTGATCGCCAGCTTGGCTTCTGGGAGACCTGCTGCACA   | 837  |
| Qy | 689  | TCGTCAATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAG  | 748  |
|    |      |  |      |
| Db | 836  | TCGTCAATTGACATCCCTATCAAGGTCTACAAGCTG-TTGCAGAGGACTGGCCATTTGGAG  | 778  |
| Qy | 749  | CTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGA   | 808  |
|    |      |  |      |
| Db | 777  | CTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGA   | 718  |
| Qy | 809  | GTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAG   | 868  |
|    |      |  |      |
| Db | 717  | GTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAG   | 658  |
| Qy | 869  | GAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTGGATTGTTGGTGGTCTCTGTGG  | 928  |
|    |      |  |      |
| Db | 657  | GAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTGGATTGTTGGTGGTCTCTGTGG  | 598  |
| Qy | 929  | TTCTGGCTGTCCCTGAAGCCATAGTTTTGATATAATTACGATGGACTACAAAGGAAGTT    | 988  |
|    |      |  |      |
| Db | 597  | TTCTGGCTGTCCCTGAAGCCATAGTTTTGATATAATTACGATGGACTACAAAGGAAGTT    | 538  |
| Qy | 989  | ATCTGCGAATCTGCTTGCTTCATCCCCTCAGAAGACAGCTTTCATGCAGTTTACAAGA     | 1048 |
|    |      |  |      |
| Db | 537  | ATCTGCGAATCTGCTTGCTTCATCCCCTCAGAAGACAGCTTTCATGCAGTTTACAAGA     | 478  |
| Qy | 1049 | CAGCAAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCAT  | 1108 |
|    |      |  |      |
| Db | 477  | CAGCAAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCAT  | 418  |
| Qy | 1109 | TT-TTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCT   | 1167 |
|    |      |  |      |
| Db | 417  | TTGTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCT   | 358  |
| Qy | 1168 | TTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTT   | 1227 |
|    |      |  |      |
| Db | 357  | TTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTT   | 298  |
| Qy | 1228 | GTCTTTGCCCTCTGCTGGCTTCCCCTTACCTCAGCAGGATTCTGAAGCTCACTCTTTAT    | 1287 |
|    |      |  |      |
| Db | 297  | GTCTTTGCCCTCTGCTGGCTTCCCCTTACCTCAGCAGGATTCTGAAGCTCACTCTTTAT    | 238  |
| Qy | 1288 | AATCAGAATGATCCCAATAGATGTGAACCTTTGAGCTTTCTGTTGGTATTGGACTATATT   | 1347 |
|    |      |  |      |
| Db | 237  | AATCAGAATGATCCCAATAGATGTGAACCTTTGAGCTTTCTGTTGGTATTGGACTATATT   | 178  |

Qy 1348 GGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAGC 1407  
 |||  
 Db 177 GGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAGC 118  
 Qy 1408 AAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCT-GCTGGTGCCAGTCATTTGAAGA 1466  
 |||  
 Db 117 AAAAGATTCAACAAGTCTTTAAGTCATGCTTATGCTGGCTGGTGCCAGTCATTTGAAGA 58  
 Qy 1467 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATG 1516  
 |||  
 Db 57 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTACAGCTAAGG 8

# RESULT 11

AL553041/c

LOCUS AL553041 1201 bp mRNA linear EST 31-MAY-2003

DEFINITION AL553041 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI072YK22 3-PRIME, mRNA sequence.

ACCESSION AL553041

VERSION AL553041.2 GI:31274855

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1201)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 15, 2001 this sequence version replaced gi:12892503.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7006.r For

more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CSODI072BF11NP1&cluster=7006.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODI072BF11NP1&cluster=7006.r). Contact :

Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CSODI072BF11NP1.

## FEATURES

Location/Qualifiers

source

1. .1201

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CSODI072YK22"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN



```

Db      294  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          ACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAA 235

Qy      4018 TGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGA 4077
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      234  TGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGA 175

Qy      4078 TTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTT-AACAACTACCTTATT 4136
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      174  TTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTTCAACAACTACCTTATT 115

Qy      4137 TTTCACTGTACAGACACTAATTCATTAAATACTAA-----TTGATTGTTTAAAAGAAA 4189
          ||||||||||||||||||||||||||||||||||| |||||||||||||||
Db      114  TTTCACTGTACAGACACTAATTCATTAAATACTCACACTCTCGCACTTGTTTAAAAGAAA 55

Qy      4190 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAG 4243
          |||||:|:|:|||||||||||||||||||||
Db      54  TATAAAKGBGMCAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAG 1

```

# RESULT 12

AL543805

LOCUS AL543805 942 bp mRNA linear EST 31-MAY-2003

DEFINITION AL543805 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI005YG20 5-PRIME, mRNA sequence.

ACCESSION AL543805

VERSION AL543805.2 GI:31265651

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 942)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 15, 2001 this sequence version replaced gi:12876284.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7006.r For more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0DI005BD10QP1&cluster=7006.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI005BD10QP1&cluster=7006.r). Contact :

Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI005BD10QP1.

## FEATURES

source

Location/Qualifiers

1. .942

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DI005YG20"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"



```
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
```

Query Match 19.8%; Score 851; DB 9; Length 942;  
Best Local Similarity 98.1%; Pred. No. 2.2e-153;  
Matches 876; Conservative 4; Mismatches 11; Indels 2; Gaps 2;

Qy 2522 TGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGATG 2581  
 |||:|||||  
 Db 771 TGCATGTAGATGATTAAMTGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGATG 830

Qy 2582 CCAGTGACCTCATAATAAAGACTGTGAACTGCCCTGGTGCAGTGTCCACATGACAAAGGGG 2641  
 |||:|||||  
 Db 831 CCAGTGACCTCATAATAAAGACTGTGAACTGCCCTGGTGCAGTGTCCACATGACAAAGGGG 890

Qy 2642 CAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATG 2694  
 |||:|||||  
 Db 891 CAGGTAGCACCTCTCTCACCCATGCTGTGGTT-AAATGGTTTCTAGCATATG 942

# RESULT 13

BQ229233

LOCUS BQ229233 891 bp mRNA linear EST 02-MAY-2002

DEFINITION AGENCOURT\_7511051 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6055288  
 5', mRNA sequence.

ACCESSION BQ229233

VERSION BQ229233.1 GI:20410633

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 891)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13315 row: e column: 17

High quality sequence stop: 696.

FEATURES Location/Qualifiers

source 1..891

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6055288"

/tissue\_type="melanotic melanoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_72"

/note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2 kb. Library constructed by Life  
 Technologies."

## ORIGIN

Query Match

19.7%; Score 848; DB 13; Length 891;

Best Local Similarity 99.1%; Pred. No. 8.3e-153;  
Matches 884; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

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Qy      2086 GTTTAGTTGTTGCATTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAG 2145
          |||
Db        1 GTTTAGTTGTTGCATTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAG 60

Qy      2146 AAAGAGCAAGGCTGTTTTTGAAAATCATTACACTTTCCTAGTAAGCCCAAACCTCAGCAT 2205
          |||
Db        61 AAAGAGCAAGGCTGTTTTTGAAAATCATTACACTTTCCTAGTAAGCCCAAACCTCAGCAT 120

Qy      2206 TCTGCAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGC 2265
          |||
Db       121 TCTGCAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGC 180

Qy      2266 CAGCTGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGT 2325
          |||
Db       181 CAGCTGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGT 240

Qy      2326 TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTT 2385
          |||
Db       241 TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTT 300

Qy      2386 TGAATCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTAT 2445
          |||
Db       301 TGAATCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTAT 360

Qy      2446 TAAAATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAAT 2505
          |||
Db       361 TAAAATCTTCTTCTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAAT 420

Qy      2506 ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT 2565
          |||
Db       421 ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT 480

Qy      2566 TTACGATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGT 2625
          |||
Db       481 TTACGATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGT 540

Qy      2626 CCACATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTC 2685
          |||
Db       541 CCACATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTC 600

Qy      2686 TAGCATATGTATAATGCTATAGTTAAATACTATTTTTTCAAATCATACAGATTAGTACA 2745
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Db       601 TAGCATATGTATAATGCTATAGTTAAATACTATTTTTTCAAATCATACAGATTAGTACA 660

Qy      2746 TTAAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAAT 2805
          |||
Db       661 TTAAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAAT 720

Qy      2806 AGAAAAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGC-AAAAGTCTTTTTGAG 2864
          |||
Db       721 AGAAAAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAAAGTCTTTTTGAG 780

Qy      2865 ACCGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAG 2924
          |||
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Db 781 ACCGTAAGAACCTCTTACCTTTGTGCGTTCTGCCTAA-TTTTAAATCTTCTAAGCAAAG 839

Qy 2925 TGCCTTAGGATAGCTTGGG-ATGAGATGTGTGTGAAAGTATGTACAAGAGAA 2975  
 |||||

Db 840 TGCCTTAGGATAGCTTGGGAATGAGATGTGTGTGAAAATATGTACAAGAAAA 891

RESULT 14

AL546465

LOCUS AL546465 1201 bp mRNA linear EST 31-MAY-2003

DEFINITION AL546465 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI030YM19 5-PRIME, mRNA sequence.

ACCESSION AL546465

VERSION AL546465.2 GI:31268299

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1201)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 15, 2001 this sequence version replaced gi:12879606.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7006.r For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI030AG10QP1&cluster=7006.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI030AG10QP1.

FEATURES

source

Location/Qualifiers

1. .1201

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DI030YM19"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 19.0%; Score 816.2; DB 9; Length 1201;

Best Local Similarity 97.2%; Pred. No. 1e-146;

Matches 854; Conservative 7; Mismatches 15; Indels 3; Gaps 3;

Qy 178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237  
 || ||

Db 219 TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 278

Qy 238 ATGCAGCCGCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297  
 |||  
 Db 279 ATGCAGCCGCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 338  
 Qy 298 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 357  
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 Db 339 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 398  
 Qy 358 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 417  
 |||  
 Db 399 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 458  
 Qy 418 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 477  
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 Db 459 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 518  
 Qy 478 CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 537  
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 Db 519 CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 578  
 Qy 538 AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGCTGCTGGGGATCATCGGGAATCC 597  
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 Db 579 AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGCTGCTGGGGATCATCGGGAATCC 638  
 Qy 598 ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC 657  
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 Db 639 ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC 698  
 Qy 658 GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC 717  
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 Db 699 GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC 758  
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 Db 759 AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA 818  
 Qy 778 CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT 837  
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 Db 819 CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT 878  
 Qy 838 CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA 897  
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 Db 879 CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTT-CAAAATGGACAGCAGTA 937  
 Qy 898 GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT 957  
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 Db 938 GAAATTGTTTTKATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTVTT 997  
 Qy 958 GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT 1017  
 |||:||||  
 Db 998 GATATAATTACGATGGACTACAAAGG-AGTTATCTGCGAATCTGCTTGCTT-MWCCSGT 1055  
 Qy 1018 CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAA 1056  
 :||| ||| : |||  
 Db 1056 YARAAGAAAGCTTTTCATGCAGTTTTACAAAAMAGCAAAA 1094

## RESULT 15

BI858627

LOCUS BI858627 972 bp mRNA linear EST 10-OCT-2001

DEFINITION 603389094F1 NIH\_MGC\_87 Homo sapiens cDNA clone IMAGE:5398054 5',  
mRNA sequence.

ACCESSION BI858627

VERSION BI858627.1 GI:15999374

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 972)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:<http://image.llnl.gov>

Plate: LLAM12014 row: 1 column: 23

High quality sequence stop: 899.

## FEATURES

source

Location/Qualifiers

1. .972

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5398054"

/tissue\_type="mammary adenocarcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_87"

/note="Organ: breast; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.383 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 18.8%; Score 808.6; DB 12; Length 972;

Best Local Similarity 96.3%; Pred. No. 3.1e-145;

Matches 903; Conservative 0; Mismatches 25; Indels 10; Gaps 7;

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Db       1 GAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCC 60

Qy      381 ACCCACTAAGACCTTATGGCCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTTCGTTGGCACC 440
          |||
Db       61 ACCCACTAAGACCTTATGGCCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTTCGTTGGCACC 120

Qy      441 TGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCTCC 500
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Db      121  |||||TGC GGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCC 180
Qy      501  CCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTGTC 560
Db      181  |||||CCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTGTC 240
Qy      561  CTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAA 620
Db      241  |||||CTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAA 300
Qy      621  GAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCT 680
Db      301  |||||GAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCT 360
Qy      681  GCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC 740
Db      361  |||||GCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC 420
Qy      741  ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCAC 800
Db      421  |||||ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCAC 480
Qy      801  TGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAG 860
Db      481  |||||TGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAG 540
Qy      861  AATTAAAGGAA-TTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTGGGTGG 919
Db      541  |||||AATTAAAGGAAC-TTGGGGTTCCAAAATGGACAGCAGTAGAAATCG-TTTGATTGGGTGG 599
Qy      920  TCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACA 979
Db      600  |||||TCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGG-TTTGATATAATTACGATGGACTACA 658
Qy      980  AAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGT 1039
Db      659  |||||AAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGT 718
Qy      1040 TTTACAAGACAGCAAAAGATTGGT-GGCTGTTTCAGTTTCTATTTCTGCTTGCCATT-GGC 1097
Db      719  |||||TTTACAAGACAGCAAAAGATTGGTGGGCTATTTCAGTTTCTATTTCTGCTTGCCATNGGGG 778
Qy      1098 CATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCAT 1157
Db      779  |||||CATCACTGCATTTTTTTTATACACTAATGACCTGTGACATGTTGAGAACGAACAGTGGCTT 838
Qy      1158 GCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTG 1217
Db      839  |||||GCAGAT--GCTTTAATGATCACCTAAAGCAGAGACGGAA---GTGGCAAACCGTCTTTTG 893
Qy      1218 CCTGGTCCCTTGCTTTTGCCCTCTGCTGGCTTCCCCTTC 1255
Db      894  |||||CCTGGTCCCTTGCTTTTGCCCTCTGCTGGGTTCCTTAC 931

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Search completed: May 14, 2004, 15:46:36

Job time : 10214.3 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 23:17:23 ; Search time 16247.7 Seconds  
(without alignments)  
11473.517 Million cell updates/sec

Title: US-09-931-157-2  
Perfect score: 4301  
Sequence: 1 gagacattccggtgggggac.....ctgggaaaaaaaaaaaaaa 4301

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*

28: em\_un:\*  
 29: em\_vi:\*  
 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pln:\*  
 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

| Result | %      |       | Query  |    | DB       | ID | Description        |
|--------|--------|-------|--------|----|----------|----|--------------------|
|        |        |       |        |    |          |    |                    |
| No.    | Score  | Match | Length |    |          |    |                    |
| 1      | 4301   | 100.0 | 4301   | 6  | AR177880 |    | AR177880 Sequence  |
| 2      | 4301   | 100.0 | 4301   | 6  | E07650   |    | E07650 cDNA encodi |
| 3      | 4286   | 99.7  | 4286   | 9  | HUMETR   |    | D90402 Homo sapien |
| 4      | 4284.4 | 99.6  | 4286   | 6  | AX548828 |    | AX548828 Sequence  |
| 5      | 4284.4 | 99.6  | 4286   | 6  | AX587707 |    | AX587707 Sequence  |
| 6      | 4284.4 | 99.6  | 4286   | 9  | S57283   |    | S57283 Homo sapien |
| 7      | 2857   | 66.4  | 2972   | 9  | D13162S7 |    | D13168 Homo sapien |
| c 8    | 2841.8 | 66.1  | 183337 | 9  | AL139002 |    | AL139002 Human DNA |
| c 9    | 2792.4 | 64.9  | 201093 | 2  | AC144750 |    | AC144750 Pan trogl |
| 10     | 2610   | 60.7  | 2720   | 11 | G06417   |    | G06417 human STS W |
| c 11   | 2550   | 59.3  | 169751 | 2  | AC130785 |    | AC130785 Papio anu |
| c 12   | 2550   | 59.3  | 185870 | 2  | AC129069 |    | AC129069 Papio anu |
| 13     | 1691.8 | 39.3  | 1873   | 6  | AR165435 |    | AR165435 Sequence  |
| 14     | 1691.8 | 39.3  | 1873   | 6  | E15242   |    | E15242 Human mRNA  |
| 15     | 1690.8 | 39.3  | 1872   | 9  | S44866   |    | S44866 ETB endothe |
| 16     | 1495.4 | 34.8  | 1719   | 9  | HUMEDNRB |    | L06623 Homo sapien |
| 17     | 1466.8 | 34.1  | 1470   | 6  | AR270640 |    | AR270640 Sequence  |
| 18     | 1466.8 | 34.1  | 1470   | 9  | HUMETSR  |    | M74921 Human endot |
| 19     | 1389   | 32.3  | 1603   | 9  | BC014472 |    | BC014472 Homo sapi |
| 20     | 1389   | 32.3  | 1632   | 6  | AX342673 |    | AX342673 Sequence  |
| 21     | 1361.4 | 31.7  | 1765   | 9  | AF114165 |    | AF114165 Homo sapi |
| 22     | 1327.4 | 30.9  | 1329   | 9  | AY275463 |    | AY275463 Homo sapi |
| 23     | 1322.6 | 30.8  | 1329   | 6  | AX280873 |    | AX280873 Sequence  |
| 24     | 1222.8 | 28.4  | 1669   | 4  | AF019072 |    | AF019072 Equus cab |
| 25     | 1220.4 | 28.4  | 1578   | 9  | HSX99250 |    | X99250 H.sapiens m |
| 26     | 1197.8 | 27.8  | 2026   | 4  | BOVEETBR |    | D90456 Bos taurus  |
| 27     | 1186   | 27.6  | 1452   | 4  | AF034530 |    | AF034530 Canis fam |
| 28     | 1113   | 25.9  | 2018   | 10 | S65355   |    | S65355 nonselectiv |
| 29     | 1110.2 | 25.8  | 1551   | 6  | E05930   |    | E05930 DNA sequenc |
| 30     | 1104.8 | 25.7  | 2115   | 10 | BC026553 |    | BC026553 Mus muscu |
| 31     | 1099.2 | 25.6  | 1958   | 6  | AX305434 |    | AX305434 Sequence  |
| 32     | 1099.2 | 25.6  | 1958   | 10 | MMU32329 |    | U32329 Mus musculu |
| 33     | 1091   | 25.4  | 1892   | 10 | RNETBREC |    | X57764 Rat mRNA fo |

|   |    |        |      |        |    |          |                    |
|---|----|--------|------|--------|----|----------|--------------------|
|   | 34 | 1091   | 25.4 | 1965   | 6  | E03623   | E03623 DNA encodin |
|   | 35 | 1086.6 | 25.3 | 1311   | 4  | AF038900 | AF038900 Equus cab |
|   | 36 | 1070.4 | 24.9 | 1321   | 6  | AR207426 | AR207426 Sequence  |
|   | 37 | 1067.6 | 24.8 | 1314   | 4  | AF276427 | AF276427 Canis fam |
|   | 38 | 1042.8 | 24.2 | 1326   | 4  | AF245469 | AF245469 Oryctolag |
| c | 39 | 931.8  | 21.7 | 135327 | 2  | AC118537 | AC118537 Felis cat |
| c | 40 | 931.8  | 21.7 | 170121 | 2  | AC123546 | AC123546 Felis cat |
| c | 41 | 922.2  | 21.4 | 192330 | 2  | AC122157 | AC122157 Canis fam |
|   | 42 | 746    | 17.3 | 1564   | 5  | AF472616 | AF472616 Gallus ga |
|   | 43 | 732.6  | 17.0 | 1041   | 5  | CCEDNRB  | X99295 C.coturnix  |
|   | 44 | 588    | 13.7 | 588    | 11 | G15922   | G15922 human STS C |
|   | 45 | 564.8  | 13.1 | 1520   | 5  | AF275636 | AF275636 Danio rer |

# ALIGNMENTS

## RESULT 1

ARI77880  
 LOCUS ARI77880 4301 bp DNA linear PAT 17-DEC-2001  
 DEFINITION Sequence 3 from patent US 6313276.  
 ACCESSION ARI77880  
 VERSION ARI77880.1 GI:17920235  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 4301)  
 AUTHORS Imura,H., Nakao,K. and Nakanishi,S.  
 TITLE Human endothelin receptor  
 JOURNAL Patent: US 6313276-A 3 06-NOV-2001;  
 FEATURES Location/Qualifiers  
 source 1. .4301  
 /organism="unknown"  
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## ORIGIN

Query Match 100.0%; Score 4301; DB 6; Length 4301;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
|    |     |   |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
|    |     |   |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
|    |     |   |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240 |
|    |     |   |     |
| Db | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240 |

Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300  
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 Db 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

Qy 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360  
 |||  
 Db 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420  
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 Db 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
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 Db 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy 481 CCACGCACCATCTCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540  
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Qy 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTCGTGCTGGGGATCATCGGGAACCTCCACA 600  
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Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
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Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 |||  
 Db 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780

Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840

Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
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 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900

Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 |||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960

Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020  
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 Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020

Qy 1021 AAGACAGCTTTCATGCAGTTTACAAGACAGCAAAGATTGGTGGCTGTTCAGTTTCTAT 1080  
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 Db 1021 AAGACAGCTTTCATGCAGTTTACAAGACAGCAAAGATTGGTGGCTGTTCAGTTTCTAT 1080

Qy 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG 1140

|    |      |  |      |
|----|------|--|------|
| Db | 1081 | <br>TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG     | 1200 |
| Db | 1141 | <br>AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC     | 1260 |
| Db | 1201 | <br>GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG     | 1320 |
| Db | 1261 | <br>AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG | 1320 |
| Qy | 1321 | AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT      | 1380 |
| Db | 1321 | <br>AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA       | 1440 |
| Db | 1381 | <br>AACCCAATTGCTCTGTATTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA      | 1500 |
| Db | 1441 | <br>TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA      | 1560 |
| Db | 1501 | <br>AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACCGAAGTCATTAA          | 1620 |
| Db | 1561 | <br>TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACCGAAGTCATTAA      | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT      | 1680 |
| Db | 1621 | <br>AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT  | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT     | 1740 |
| Db | 1681 | <br>TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT     | 1800 |
| Db | 1741 | <br>TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT     | 1860 |
| Db | 1801 | <br>TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT       | 1920 |
| Db | 1861 | <br>TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT   | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG     | 1980 |
|    |      |  |      |

Db 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG 1980  
 Qy 1981 AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT 2040  
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 Db 1981 AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT 2040  
 Qy 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT 2100  
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 Db 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT 2100  
 Qy 2101 TTTTCGGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT 2160  
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 Db 2101 TTTTCGGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT 2160  
 Qy 2161 TTTTGAAAATCATTACACTTTTCTACTAGAAGCCCCAACCTCAGCATTCTGCAATATGTAAC 2220  
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 Db 2161 TTTTGAAAATCATTACACTTTTCTACTAGAAGCCCCAACCTCAGCATTCTGCAATATGTAAC 2220  
 Qy 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA 2280  
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 Db 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA 2280  
 Qy 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTGAGTAAAGATCAAACCTCA 2340  
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 Db 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTGAGTAAAGATCAAACCTCA 2340  
 Qy 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA 2400  
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 Db 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA 2400  
 Qy 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT 2460  
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 Db 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT 2460  
 Qy 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 Qy 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Qy 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
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 Db 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Qy 2641 GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
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 Db 2641 GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 Qy 2701 GCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760  
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 Db 2701 GCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760  
 Qy 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
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 Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820

|    |      |  |      |
|----|------|--|------|
| Qy | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGGAGACCGTAAGAACCTCTT   | 2880 |
|    |      |  |      |
| Db | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGGAGACCGTAAGAACCTCTT   | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT    | 2940 |
|    |      |  |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT    | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
|    |      |  |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATCTTAGCCTAACGTTTCGTCATTGCCT   | 3060 |
|    |      |  |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATCTTAGCCTAACGTTTCGTCATTGCCT   | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
|    |      |  |      |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCCA    | 3180 |
|    |      |  |      |
| Db | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCCA    | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
|    |      |  |      |
| Db | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 3300 |
|    |      |  |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
|    |      |  |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA    | 3480 |
|    |      |  |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA    | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
|    |      |  |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT    | 3600 |
|    |      |  |      |
| Db | 3541 | TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT    | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
|    |      |  |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |

Qy 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
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 Db 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
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 Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
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 Qy 3841 CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
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 Db 3841 CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
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 Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
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 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
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 Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
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 Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
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 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
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 Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140  
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 Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
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 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
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 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
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 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAA 4301  
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 Db 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAA 4301  
 |||

# RESULT 2

E07650

LOCUS E07650 4301 bp RNA linear PAT 29-SEP-1997

DEFINITION cDNA encoding endothelin receptor, ETB-receptor.

ACCESSION E07650

VERSION E07650.1 GI:2175785

KEYWORDS JP 1994157595-A/2.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4301)



AUTHORS Imura,H., Nakao,I. and Nakanishi,S.  
 TITLE HUMAN ENDOTHELIN RECEPTOR  
 JOURNAL Patent: JP 1994157595-A 2 03-JUN-1994;  
 SHIONOGI & CO LTD  
 COMMENT OS Homo sapiens (human)  
 PN JP 1994157595-A/2  
 PD 03-JUN-1994  
 PF 12-JUL-1991 JP 1991172828  
 PI IMURA HIROO, NAKAO ICHIKAZU, NAKANISHI SHIGETADA PC  
 C07K13/00,C12N5/10,C12N15/12,C12P21/02,(C12N5/10,C12R1:91), PC  
 (C12P21/02,  
 PC C12R1:91);  
 CC strandedness: Double;  
 CC topology: Linear;  
 CC hypothetical: No;  
 CC anti-sense: No;  
 FH Key Location/Qualifiers  
 FT source 1. .4301  
 FT /organism='Homo sapiens'  
 FT /tissue\_type='placenta'  
 FT /clone='pHETBR31 and pHTBR34' FT 5'UTR  
 1. .237  
 FT CDS 238. .1566  
 FT /product='endothelin receptor,ETB-receptor' FT  
 3'UTR 1567. .4301  
 FT polyA\_signal 4258. .4263  
 FT polyA\_signal 3638. .3643  
 FT polyA\_signal 3134. .3139  
 FT polyA\_signal 2594. .2599  
 FT polyA\_signal 1689. .1694.  
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 source 1. .4301  
 /organism="Homo sapiens"  
 /mol\_type="genomic RNA"  
 /db\_xref="taxon:9606"

# ORIGIN

Query Match 100.0%; Score 4301; DB 6; Length 4301;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
|    |     |  |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
|    |     |  |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA | 180 |
|    |     |  |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG | 240 |
|    |     |  |     |
| Db | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG | 240 |

|    |      |   |      |
|----|------|---|------|
| Qy | 241  | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGCCTG | 300  |
|    |      |   |      |
| Db | 241  | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGCCTG | 300  |
| Qy | 301  | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360  |
|    |      |   |      |
| Db | 301  | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360  |
| Qy | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420  |
|    |      |   |      |
| Db | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420  |
| Qy | 421  | CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480  |
|    |      |   |      |
| Db | 421  | CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480  |
| Qy | 481  | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540  |
|    |      |   |      |
| Db | 481  | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540  |
| Qy | 541  | TACATCAACACGGTTGTGTCTGCTTGTGTTCTGCTGGGGATCATCGGGAACCTCCACA    | 600  |
|    |      |   |      |
| Db | 541  | TACATCAACACGGTTGTGTCTGCTTGTGTTCTGCTGGGGATCATCGGGAACCTCCACA    | 600  |
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660  |
|    |      |   |      |
| Db | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660  |
| Qy | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720  |
|    |      |   |      |
| Db | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720  |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780  |
|    |      |   |      |
| Db | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780  |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
|    |      |   |      |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
|    |      |   |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
|    |      |   |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
|    |      |   |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
|    |      |   |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
|    |      |   |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
|    |      |   |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
|    |      |   |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
|    |      |   |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
| Qy | 1321 | AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
|    |      |   |      |
| Db | 1321 | AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
|    |      |   |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
|    |      |   |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
|    |      |   |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
|    |      |   |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT   | 1680 |
|    |      |   |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
|    |      |   |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA  | 1920 |
|    |      |   |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA  | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG | 1980 |

|    |      |   |      |
|----|------|---|------|
| Db | 1921 | <br>AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAAGCTTTTAAATG  | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAAGCTTTTCAATTAATAT     | 2040 |
| Db | 1981 | <br>AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAAGCTTTTCAATTAATAT | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT      | 2100 |
| Db | 2041 | <br>TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT      | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTGTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC     | 2220 |
| Db | 2161 | <br>TTTGTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA      | 2280 |
| Db | 2221 | <br>CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTAAAGATCAAACCTCA     | 2340 |
| Db | 2281 | <br>TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTAAAGATCAAACCTCA | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA       | 2400 |
| Db | 2341 | <br>CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT      | 2460 |
| Db | 2401 | <br>CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT  | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCTGTAATACTTACCTACATACA          | 2520 |
| Db | 2461 | <br>TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCTGTAATACTTACCTACATACA      | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT      | 2580 |
| Db | 2521 | <br>CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG       | 2640 |
| Db | 2581 | <br>GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT       | 2700 |
| Db | 2641 | <br>GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT   | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG     | 2760 |
| Db | 2701 | <br>GCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG      | 2820 |
|    |      |   |      |

Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 Qy 2821 ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
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 Db 2821 ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
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 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
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 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATCTTAGCCTAACGTTTCGTCATTGCCT 3060  
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 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
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 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301  
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 Db 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301  
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# RESULT 3

HUMETR

LOCUS HUMETR 4286 bp mRNA linear PRI 18-DEC-2002

DEFINITION Homo sapiens ETR mRNA for endothelin receptor, complete cds.

ACCESSION D90402

VERSION D90402.1 GI:219651

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4286)  
 AUTHORS Ogawa,Y., Nakao,K., Arai,H., Nakagawa,O., Hosoda,K., Suga,S.,  
 Nakanishi,S. and Imura,H.  
 TITLE Molecular cloning of a non-isopeptide-selective human endothelin  
 receptor  
 JOURNAL Biochem. Biophys. Res. Commun. 178 (1), 248-255 (1991)  
 MEDLINE 91298956  
 PUBMED 1648908  
 COMMENT Data kindly submitted in computer readable form by: Kazuwa Nakao  
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 Sakyo-ku, Kyoto 606  
 Japan  
 Phone: 81-75-751-3170  
 Fax: 81-75-771-9452.

FEATURES Location/Qualifiers  
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# ORIGIN

Query Match 99.7%; Score 4286; DB 9; Length 4286;  
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 Matches 4286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
|    |     |   |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
|    |     |   |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
|    |     |   |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |

Qy 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
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 Db 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300  
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Qy 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360  
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Qy 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
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Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
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Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 780  
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Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
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Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
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 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900

Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
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 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960

Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020  
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Qy 1021 AAGACAGCTTTCATGCAGTTTACAAGACAGCAAAGATTGGTGGCTGTTCAAGTTTCTAT 1080



|    |      |  |      |
|----|------|--|------|
| Db | 1021 | <br>AAGACAGCTTTTCATGCAGTTTACAAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG       | 1140 |
| Db | 1081 | <br>TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG       | 1200 |
| Db | 1141 | <br>AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC       | 1260 |
| Db | 1201 | <br>GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG       | 1320 |
| Db | 1261 | <br>AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT       | 1380 |
| Db | 1321 | <br>AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA        | 1440 |
| Db | 1381 | <br>AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA        | 1500 |
| Db | 1441 | <br>TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA        | 1560 |
| Db | 1501 | <br>AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAAGTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA           | 1620 |
| Db | 1561 | <br>TCTTGAAAGAAGAAGTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA       | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAGTATGTATTTGCACAGCACACTAT         | 1680 |
| Db | 1621 | <br>AACAAAATGAAACATTTGCCAAAACAAAACAAAAGTATGTATTTGCACAGCACACTAT     | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT       | 1740 |
| Db | 1681 | <br>TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT       | 1800 |
| Db | 1741 | <br>TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAAGTCCAGGATATTCACACAACACT        | 1860 |
| Db | 1801 | <br>TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAAGTCCAGGATATTCACACAACACT    | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA       | 1920 |
|    |      |  |      |

|    |      |   |      |
|----|------|---|------|
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
| Db | 2161 | TTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT  | 2460 |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT  | 2460 |
| Qy | 2461 | TCATATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA   | 2520 |
| Db | 2461 | TCATATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA   | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
| Db | 2581 | GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT | 2700 |
| Db | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |

|    |      |  |      |
|----|------|--|------|
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTGTAAATAGCCAATAGAAAAGTTTGCTTG    | 2820 |
|    |      |  |      |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTGTAAATAGCCAATAGAAAAGTTTGCTTG    | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAAGTCTTTTGAGACCGTAAGAACCTCTT   | 2880 |
|    |      |  |      |
| Db | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAAGTCTTTTGAGACCGTAAGAACCTCTT   | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
|    |      |  |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
|    |      |  |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
|    |      |  |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
|    |      |  |      |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA    | 3180 |
|    |      |  |      |
| Db | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA    | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
|    |      |  |      |
| Db | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCA   | 3300 |
|    |      |  |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCA   | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTACACACCATATGGATTCTATTTATAAATCACCC    | 3360 |
|    |      |  |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTACACACCATATGGATTCTATTTATAAATCACCC    | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
|    |      |  |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
|    |      |  |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
|    |      |  |      |
| Db | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |

QY 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660  
 QY 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
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 Db 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 QY 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780  
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 Db 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780  
 QY 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
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 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 QY 3841 CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3841 CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 QY 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
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 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 QY 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 QY 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 QY 4081 TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 4140  
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 Db 4081 TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 4140  
 QY 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 QY 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
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 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 QY 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 ||||||||||||||||||||||||||||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 4

AX548828

LOCUS

AX548828

4286 bp

DNA

linear

PAT 26-NOV-2002

DEFINITION

Sequence 113 from Patent WO02061087.

ACCESSION

AX548828

VERSION

AX548828.1 GI:25813723

KEYWORDS

.

SOURCE

Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Burmer, G.C., Roush, C.L. and Brown, J.P.

TITLE Antigenic peptides, such as for G protein-coupled receptors  
(GPCRs), antibodies thereto, and systems for identifying such  
antigenic peptides

JOURNAL Patent: WO 02061087-A 113 08-AUG-2002;  
Lifespan Biosciences, Inc. (US)

FEATURES Location/Qualifiers

source 1. .4286  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

# ORIGIN

Query Match 99.6%; Score 4284.4; DB 6; Length 4286;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
|    |     |  |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
|    |     |  |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA | 180 |
|    |     |  |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240 |
|    |     |  |     |
| Db | 181 | AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240 |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG | 300 |
|    |     |  |     |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA | 360 |
|    |     |  |     |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT | 420 |
|    |     |  |     |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT | 420 |
| Qy | 421 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
|    |     |  |     |
| Db | 421 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |
|    |     |  |     |
| Db | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |

|    |      |  |      |
|----|------|--|------|
| Qy | 541  | TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA  | 600  |
|    |      |  |      |
| Db | 541  | TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA  | 600  |
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
|    |      |  |      |
| Db | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Qy | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
|    |      |  |      |
| Db | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
|    |      |  |      |
| Db | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
|    |      |  |      |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
|    |      |  |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT    | 960  |
|    |      |  |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT    | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG  | 1020 |
|    |      |  |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
|    |      |  |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
|    |      |  |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
|    |      |  |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTC    | 1260 |
|    |      |  |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTC    | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
|    |      |  |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
|    |      |  |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA  | 1440 |

|    |      |  |      |
|----|------|--|------|
| Db | 1381 | <br>AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAACTGCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA       | 1500 |
| Db | 1441 | <br>TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA       | 1560 |
| Db | 1501 | <br>AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA       | 1620 |
| Db | 1561 | <br>TCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA   | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT        | 1680 |
| Db | 1621 | <br>AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT    | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT       | 1740 |
| Db | 1681 | <br>TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT       | 1800 |
| Db | 1741 | <br>TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT       | 1860 |
| Db | 1801 | <br>TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA      | 1920 |
| Db | 1861 | <br>TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA  | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG       | 1980 |
| Db | 1921 | <br>AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT         | 2040 |
| Db | 1981 | <br>AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT     | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT       | 2100 |
| Db | 2041 | <br>TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT       | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTCACTAGAAAGCCCAAACCTCAGCATTCTGCAATATGTAAC     | 2220 |
| Db | 2161 | <br>TTTTGAAAATCATTACACTTTTCACTAGAAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA       | 2280 |
|    |      |  |      |

|    |      |   |      |
|----|------|---|------|
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTTAAGATCAAACCTCA | 2340 |
|    |      |   |      |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTTAAGATCAAACCTCA | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
|    |      |   |      |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTT     | 2460 |
|    |      |   |      |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTT     | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
|    |      |   |      |
| Db | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
|    |      |   |      |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
|    |      |   |      |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT   | 2700 |
|    |      |   |      |
| Db | 2641 | GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT   | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
|    |      |   |      |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
|    |      |   |      |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT | 2880 |
|    |      |   |      |
| Db | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
|    |      |   |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
|    |      |   |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
|    |      |   |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |
|    |      |   |      |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |



|    |      |   |      |
|----|------|---|------|
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA   | 3180 |
|    |      |   |      |
| Db | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA   | 3180 |
| Qy | 3181 | ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG     | 3240 |
|    |      |   |      |
| Db | 3181 | ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG     | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA   | 3300 |
|    |      |   |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA   | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
|    |      |   |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
| Qy | 3361 | ACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |   |      |
| Db | 3361 | ACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
|    |      |   |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 3540 |
|    |      |   |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
|    |      |   |      |
| Db | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT  | 3660 |
|    |      |   |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT  | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
|    |      |   |      |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
|    |      |   |      |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
|    |      |   |      |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
|    |      |   |      |
| Db | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
|    |      |   |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |

Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
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 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140  
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 Db 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140  
 Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
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 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 ||||||||||||||||||||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 5

AX587707

LOCUS AX587707 4286 bp DNA linear PAT 10-JAN-2003

DEFINITION Sequence 177 from Patent WO0246467.

ACCESSION AX587707

VERSION AX587707.1 GI:28212378

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1

AUTHORS Bertucci,F., Houlgatte,R., Birnbaum,D., Nguyen,C., Viens,P. and  
 Fert,V.

TITLE Gene expression profiling of primary breast carcinomas using arrays  
 of candidate genes

JOURNAL Patent: WO 0246467-A 177 13-JUN-2002;  
 Ipsogen (FR)

FEATURES Location/Qualifiers

source 1. .4286

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="primer"

misc\_feature 1. .4286

/note="endothelin receptor type b (EDNRB) gene."

ORIGIN

Query Match 99.6%; Score 4284.4; DB 6; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGACATTCCGGTGGGGGACTCTGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

|    |     |   |     |
|----|-----|---|-----|
| Db | 1   |   | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
| Db | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCCTG  | 300 |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCCTG  | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTCCAACGCCAGT   | 420 |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTCCAACGCCAGT   | 420 |
| Qy | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Db | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA    | 540 |
| Db | 481 | CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA    | 540 |
| Qy | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA | 600 |
| Db | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA | 600 |
| Qy | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
| Db | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
| Qy | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
| Db | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
| Qy | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG | 780 |
| Db | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG | 780 |
| Qy | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840 |
| Db | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840 |
| Qy | 841 | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900 |

Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCTAAATGGACAGCAGTAGAA 900  
 Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020  
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 Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020  
 Qy 1021 AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1021 AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080  
 Qy 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 Qy 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 Qy 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260  
 Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG 1320  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG 1320  
 Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
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 Db 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 Qy 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTGCTTTAAGTCATGCTTA 1440  
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 Db 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTGCTTTAAGTCATGCTTA 1440  
 Qy 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500  
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 Db 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500  
 Qy 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA 1560  
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 Db 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA 1560  
 Qy 1561 TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA 1620  
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 Db 1561 TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA 1620  
 Qy 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT 1680  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT 1680  
 Qy 1681 TAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT 1740  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1681 TAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT 1740

|    |      |   |      |
|----|------|---|------|
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTATTTT     | 1920 |
|    |      |   |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTATTTT     | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACCTTTTAAATG | 1980 |
|    |      |   |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACCTTTTAAATG | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
|    |      |   |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
|    |      |   |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
|    |      |   |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
|    |      |   |      |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
|    |      |   |      |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
|    |      |   |      |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTT    | 2460 |
|    |      |   |      |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTT    | 2460 |
| Qy | 2461 | TCATATCGTAGCTTAAACTCTGTTTGGTTTGTGCATCTGTAAATACTTACCTACATACA   | 2520 |
|    |      |   |      |
| Db | 2461 | TCATATCGTAGCTTAAACTCTGTTTGGTTTGTGCATCTGTAAATACTTACCTACATACA   | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
|    |      |   |      |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |

Qy 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
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 Db 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640

Qy 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
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 Db 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700

Qy 2701 GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG 2760  
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 Db 2701 GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG 2760

Qy 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
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 Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820

Qy 2821 ACATGGTGCTTTTCTTTTCATCTAGAGGC AAAACTGCTTTTGTAGACCGTAAGAACCTCTT 2880  
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Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
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 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940

Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
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 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000

Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT 3060  
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 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT 3060

Qy 3061 CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAACACAGTGCAATGTTCTCA 3120  
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 Db 3061 CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAACACAGTGCAATGTTCTCA 3120

Qy 3121 GAGTGACTTTGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
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 Db 3121 GAGTGACTTTGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180

Qy 3181 ATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
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 Db 3181 ATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240

Qy 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
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 Db 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300

Qy 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 |||  
 Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360

Qy 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 |||  
 Db 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT 3420

Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480

|    |      |  |      |
|----|------|--|------|
| Db | 3421 | <br>CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA         | 3540 |
| Db | 3481 | <br>TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
| Qy | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT      | 3600 |
| Db | 3541 | <br>TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAGTGGCTT       | 3660 |
| Db | 3601 | <br>TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAGTGGCTT   | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT        | 3720 |
| Db | 3661 | <br>TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTCAAACATGT          | 3780 |
| Db | 3721 | <br>TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTCAAACATGT      | 3780 |
| Qy | 3781 | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA       | 3840 |
| Db | 3781 | <br>TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
| Qy | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT        | 3900 |
| Db | 3841 | <br>CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA       | 3960 |
| Db | 3901 | <br>GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 3960 |
| Qy | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT        | 4020 |
| Db | 3961 | <br>GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT    | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT       | 4080 |
| Db | 4021 | <br>AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAAACAACTACCTTATTTTTC     | 4140 |
| Db | 4081 | <br>TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAAACAACTACCTTATTTTTC | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA       | 4200 |
| Db | 4141 | <br>ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA   | 4200 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT       | 4260 |
| Db | 4201 | <br>CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT   | 4260 |
| Qy | 4261 | AAAATGCCACATTTCTGGTCTCTGGG   | 4286 |
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## RESULT 6

\$57283

|       |        |         |      |        |                 |
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| LOCUS | S57283 | 4286 bp | mRNA | linear | PRI 18-MAR-2002 |
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DEFINITION Homo sapiens endothelin ET-B receptor mRNA, complete cds.

ACCESSION S57283

VERSION S57283.1 GI:298321

## KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4286)

REFERENCE 1 (bases 1 to 1200)  
AUTHORS Arai, H., Nakao, K., Hosoda, K., Ogawa, Y., Nakagawa, O., Komatsu, Y. and Imura, H.

|       |  |
|-------|--|
| TITLE | Molecular cloning of human endothelin receptors and their expression in vascular endothelial cells and smooth muscle cells |
|-------|--|

JOURNAL Jpn. Circ. J. 56 Suppl 5, 1303-1307 (1992)

MEDLINE 93180293

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| PUBMED | 1291713 |
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REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 128424] from the original journal article. This sequence comes from Fig. 5.

## FEATURES

Location/Qualifiers

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CDS

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AVEIVLIWVVSVVLAVPEAIGFDIITMDYKGSYLRI CLLHPVQKTA FMQFYKTAKDWW

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

QY 61 AGGTAGGCATTTGCCCGGTGGGACGCCCTTGCCAGAGCAGTGTGTGGCAGGCCCGCGTGG 120



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|----|-----|---|-----|
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCCGTGG | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
|    |     |   |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240 |
|    |     |   |     |
| Db | 181 | AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240 |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300 |
|    |     |   |     |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
|    |     |   |     |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
|    |     |   |     |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
| Qy | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
|    |     |   |     |
| Db | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Qy | 481 | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |
|    |     |   |     |
| Db | 481 | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |
| Qy | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCCACA  | 600 |
|    |     |   |     |
| Db | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCCACA  | 600 |
| Qy | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
|    |     |   |     |
| Db | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
| Qy | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
|    |     |   |     |
| Db | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
| Qy | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |
|    |     |   |     |
| Db | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |
| Qy | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840 |
|    |     |   |     |
| Db | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840 |
| Qy | 841 | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900 |
|    |     |   |     |
| Db | 841 | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900 |
| Qy | 901 | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960 |
|    |     |   |     |
| Db | 901 | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960 |

|    |      |   |      |
|----|------|---|------|
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
|    |      |   |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTAT | 1080 |
|    |      |   |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
|    |      |   |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
|    |      |   |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
|    |      |   |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG | 1320 |
|    |      |   |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
|    |      |   |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
|    |      |   |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
|    |      |   |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
|    |      |   |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
|    |      |   |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT   | 1680 |
|    |      |   |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
|    |      |   |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
|    |      |   |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
|    |      |   |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
|    |      |   |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
|    |      |   |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
|    |      |   |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
|    |      |   |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
|    |      |   |      |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
|    |      |   |      |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
|    |      |   |      |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTT   | 2460 |
|    |      |   |      |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTT   | 2460 |
| Qy | 2461 | TCATATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA    | 2520 |
|    |      |   |      |
| Db | 2461 | TCATATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA    | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
|    |      |   |      |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
|    |      |   |      |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Qy | 2641 | GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT   | 2700 |

|    |      |   |      |
|----|------|---|------|
| Db | 2641 | GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGAGACCGTAAGAACCTCTT   | 2880 |
| Db | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGAGACCGTAAGAACCTCTT   | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |
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| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA  | 3180 |
| Db | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA  | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
| Db | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
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| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
| Qy | 3361 | ACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Db | 3361 | ACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
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| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 3540 |

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Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

LOCUS D13162S7 2972 bp DNA linear PRI 12-OCT-2002  
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 VERSION D13168.1 GI:285924  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2972)  
 AUTHORS Arai,H., Nakao,K., Takaya,K., Hosoda,K., Ogawa,Y., Nakanishi,S. and  
 Imura,H.  
 TITLE The human endothelin-B receptor gene. Structural organization and  
 chromosomal assignment  
 JOURNAL J. Biol. Chem. 268 (5), 3463-3470 (1993)  
 MEDLINE 93155196  
 PUBMED 8429023  
 REFERENCE 2 (bases 1 to 2972)  
 AUTHORS Arai,H.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-SEP-1992) Hiroshi Arai, Kyoto University School of  
 Medicine, Second Division, Department of Medicine; 54 Shogoin,  
 Kawahara-cho, Sakyo-ku, Kyoto, Kyoto 606, Japan  
 (Tel:81-75-751-3170, Fax:81-75-771-9452)  
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 KLLAEDWPFGAEMCKLV PFIQKASV GITVLSLCALSIDRYAVASWSRIKGIGVPKWT  
 AVEIVLIWVSVVLAVPEAIGFDIITMDYKGSYLRLCLHPVQKTA FMQFYKTAKDWW  
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 CWLPLHLSRILKLTLYNQNDPNRCELLSFLLVLDYIGINMASLNSCINPIALYLVSKR  
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/note="G protein-coupled receptor"  
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ORIGIN

Query Match 66.4%; Score 2857; DB 9; Length 2972;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2857; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Qy | 1490 | AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA | 1549 |
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| Db | 69   | AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA | 128  |
| Qy | 1550 | AATACAGCTCATCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACC      | 1609 |
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| Db | 369  | AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT | 428  |
| Qy | 1850 | CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG | 1909 |
|    |      |  |      |
| Db | 429  | CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG | 488  |
| Qy | 1910 | ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA | 1969 |
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| Db | 489  | ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA | 548  |
| Qy | 1970 | ACTTTTAAATGAAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTT   | 2029 |
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| Db | 549  | ACTTTTAAATGAAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTT   | 608  |
| Qy | 2030 | TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAATGAGAGAGCAGTTT  | 2089 |
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| Db | 609  | TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAATGAGAGAGCAGTTT  | 668  |
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 Db 1389 AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT 1448

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Qy 2990 GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT 3049



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| Db | 1569 |  | GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT  | 1628 |
| Qy | 3050 |  | CGTCATTGCCTCGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTG    | 3109 |
| Db | 1629 |  | CGTCATTGCCTCGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTG    | 1688 |
| Qy | 3110 |  | CAATGTTCTCAGAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA  | 3169 |
| Db | 1689 |  | CAATGTTCTCAGAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA  | 1748 |
| Qy | 3170 |  | AATATGCCCAAATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA    | 3229 |
| Db | 1749 |  | AATATGCCCAAATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA    | 1808 |
| Qy | 3230 |  | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA   | 3289 |
| Db | 1809 |  | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA   | 1868 |
| Qy | 3290 |  | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT  | 3349 |
| Db | 1869 |  | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT  | 1928 |
| Qy | 3350 |  | ATAAATCACCCACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT | 3409 |
| Db | 1929 |  | ATAAATCACCCACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT | 1988 |
| Qy | 3410 |  | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA  | 3469 |
| Db | 1989 |  | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA  | 2048 |
| Qy | 3470 |  | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT  | 3529 |
| Db | 2049 |  | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT  | 2108 |
| Qy | 3530 |  | GAATTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC   | 3589 |
| Db | 2109 |  | GAATTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC   | 2168 |
| Qy | 3590 |  | TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA  | 3649 |
| Db | 2169 |  | TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA  | 2228 |
| Qy | 3650 |  | TTCAGTGGCTTTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA    | 3709 |
| Db | 2229 |  | TTCAGTGGCTTTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA    | 2288 |
| Qy | 3710 |  | ACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT   | 3769 |
| Db | 2289 |  | ACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT   | 2348 |
| Qy | 3770 |  | TCAAAACATGTTTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA  | 3829 |
| Db | 2349 |  | TCAAAACATGTTTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA  | 2408 |
| Qy | 3830 |  | CATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTAT    | 3889 |
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Db 2469 CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC 2528

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Db 2529 AAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA 2588

Qy 4010 TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA 4069  
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Db 2589 TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA 2648

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Db 2649 GTTACTGATTTTTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAAACAATA 2708

Qy 4130 CCTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA 4189  
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Db 2709 CCTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA 2768

Qy 4190 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 4249  
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Db 2769 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 2828

Qy 4250 GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 4286  
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# RESULT 8

AL139002/c

LOCUS AL139002 183337 bp DNA linear PRI 28-JAN-2001

DEFINITION Human DNA sequence from clone RP11-318G21 on chromosome 13q22.2-31.1, complete sequence.

ACCESSION AL139002

VERSION AL139002.18 GI:12597038

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 183337)

AUTHORS Wall,M.

TITLE Direct Submission

JOURNAL Submitted (28-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Jan 29, 2001 this sequence version replaced gi:12584355. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria

as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr13> RP11-318G21 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACe3.6 This sequence is the entire insert of clone RP11-318G21 The true left end of clone RP11-267I18 is at 125528 in this sequence.

| FEATURES      | Location/Qualifiers   |
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| source        | 1. .183337<br>/organism="Homo sapiens"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:9606"<br>/chromosome="13"<br>/map="q22.2-31.1"<br>/clone="RP11-318G21"<br>/clone_lib="RPCI-11.2" |
| repeat_region | 3. .454<br>/note="L1MC5 repeat: matches 7127. .7575 of consensus"   |
| repeat_region | 1216. .1308<br>/note="HAL1 repeat: matches 1475. .1563 of consensus"  |
| repeat_region | 1309. .1597<br>/note="AluJb repeat: matches 1. .297 of consensus"   |
| repeat_region | 1598. .2044<br>/note="HAL1 repeat: matches 1003. .1475 of consensus"  |
| repeat_region | 2148. .2276<br>/note="L2 repeat: matches 2620. .2749 of consensus"  |
| repeat_region | 2330. .2378<br>/note="L2 repeat: matches 2442. .2492 of consensus"  |
| repeat_region | 3915. .4224<br>/note="AluY repeat: matches 1. .306 of consensus"  |
| repeat_region | 4617. .4750<br>/note="67 copies 2 mer cc 61% conserved"   |
| repeat_region | 4648. .4727<br>/note="20 copies 4 mer cctt 78% conserved"   |
| repeat_region | 4729. .4784<br>/note="14 copies 4 mer tcct 78% conserved"   |
| repeat_region | 5431. .5736<br>/note="AluSx repeat: matches 1. .305 of consensus"   |
| repeat_region | 11990. .12273<br>/note="AluSx repeat: matches 9. .292 of consensus"   |
| repeat_region | 12589. .12809<br>/note="MIR repeat: matches 7. .234 of consensus"   |
| repeat_region | 13390. .13519<br>/note="L2 repeat: matches 2410. .2548 of consensus"  |
| repeat_region | 14630. .14978   |

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| repeat_region | 15092. .15580 | /note="THE1B repeat: matches 1. .360 of consensus"     |
| repeat_region | 15581. .16095 | /note="L1MB1 repeat: matches 5656. .6116 of consensus" |
| repeat_region | 16096. .16549 | /note="L1PA7 repeat: matches 5629. .6143 of consensus" |
| repeat_region | 16731. .16777 | /note="L1MB1 repeat: matches 5188. .5656 of consensus" |
| repeat_region | 16778. .17137 | /note="MIR repeat: matches 35. .78 of consensus"       |
| repeat_region | 17138. .17273 | /note="THE1C repeat: matches 1. .371 of consensus"     |
| repeat_region | 17374. .17484 | /note="MIR repeat: matches 78. .226 of consensus"      |
| repeat_region | 17485. .17777 | /note="MIR repeat: matches 26. .158 of consensus"      |
| repeat_region | 17778. .17815 | /note="AluSc repeat: matches 1. .290 of consensus"     |
| repeat_region | 18981. .19048 | /note="MIR repeat: matches 158. .191 of consensus"     |
| repeat_region | 19447. .19589 | /note="34 copies 2 mer tt 66% conserved"               |
| repeat_region | 19843. .20162 | /note="MIR repeat: matches 131. .262 of consensus"     |
| repeat_region | 20866. .21198 | /note="MER33 repeat: matches 1. .324 of consensus"     |
| repeat_region | 21742. .21878 | /note="MER44A repeat: matches 3. .333 of consensus"    |
| repeat_region | 22214. .22310 | /note="MIR repeat: matches 9. .154 of consensus"       |
| repeat_region | 22321. .22418 | /note="MIR repeat: matches 164. .260 of consensus"     |
| repeat_region | 22390. .22715 | /note="L1MB8 repeat: matches 6078. .6171 of consensus" |
| misc_feature  | 22419. .22730 | /note="Sequence from AC018674 sequenced by WUGSC."     |
| repeat_region | 22731. .23714 | /note="AluY repeat: matches 1. .311 of consensus"      |
| repeat_region | 23715. .24008 | /note="L1MB8 repeat: matches 5130. .6078 of consensus" |
| repeat_region | 24009. .24264 | /note="AluSg repeat: matches 1. .294 of consensus"     |
| repeat_region | 24265. .24569 | /note="L1MB8 repeat: matches 4884. .5130 of consensus" |
| repeat_region | 24570. .25577 | /note="AluY repeat: matches 1. .305 of consensus"      |
| repeat_region | 25582. .25635 | /note="L1MB8 repeat: matches 3786. .4884 of consensus" |
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| repeat_region | 26572. .26750 | /note="MSTA repeat: matches 1. .347 of consensus"      |
| repeat_region | 26752. .27066 | /note="AluY repeat: matches 129. .307 of consensus"    |
| repeat_region | 27067. .27134 | /note="AluY repeat: matches 1. .311 of consensus"      |
| repeat_region |               | /note="MSTA repeat: matches 347. .371 of consensus"    |

|               |  |
|---------------|--|
| repeat_region | 27963. .28006<br>/note="22 copies 2 mer tt 75% conserved"                |
| repeat_region | 28916. .29282<br>/note="MER39 repeat: matches 13. .381 of consensus"     |
| repeat_region | 29282. .29517<br>/note="MER39b repeat: matches 327. .579 of consensus"   |
| repeat_region | 30210. .30526<br>/note="AluJo repeat: matches 1. .303 of consensus"      |
| repeat_region | 31423. .31572<br>/note="L1PA13 repeat: matches 6005. .6155 of consensus" |
| repeat_region | 31587. .31624<br>/note="19 copies 2 mer tt 86% conserved"                |
| repeat_region | 32103. .32181<br>/note="ORSL repeat: matches 390. .467 of consensus"     |
| repeat_region | 33878. .34312<br>/note="MER57A repeat: matches 1. .433 of consensus"     |
| repeat_region | 36673. .36768<br>/note="LTR37A repeat: matches 81. .172 of consensus"    |
| repeat_region | 36769. .37066<br>/note="AluSq repeat: matches 1. .296 of consensus"      |
| repeat_region | 37067. .37300<br>/note="LTR37A repeat: matches 172. .424 of consensus"   |
| repeat_region | 39470. .39501<br>/note="16 copies 2 mer tt 90% conserved"                |
| repeat_region | 41434. .42607<br>/note="L1M4 repeat: matches -258. .888 of consensus"    |
| repeat_region | 42744. .43220<br>/note="L1M4 repeat: matches 1085. .1580 of consensus"   |
| repeat_region | 43703. .44007<br>/note="AluJb repeat: matches 1. .305 of consensus"      |
| repeat_region | 44019. .44180<br>/note="L1MD1 repeat: matches 6044. .6211 of consensus"  |
| repeat_region | 44183. .44485<br>/note="AluJo repeat: matches 1. .300 of consensus"      |
| repeat_region | 44486. .44611<br>/note="L1MD2 repeat: matches 5949. .6066 of consensus"  |
| repeat_region | 45256. .45430<br>/note="MER5B repeat: matches 1. .178 of consensus"      |
| repeat_region | 45588. .45669<br>/note="MER5A repeat: matches 109. .188 of consensus"    |
| repeat_region | 46919. .47084<br>/note="MIR repeat: matches 94. .260 of consensus"       |
| repeat_region | 47873. .47902<br>/note="15 copies 2 mer tg 90% conserved"                |
| repeat_region | 49906. .49933<br>/note="7 copies 4 mer tgtg 96% conserved"               |
| repeat_region | 50452. .50507<br>/note="LTR37A repeat: matches 128. .184 of consensus"   |
| repeat_region | 51786. .51829<br>/note="MER74A repeat: matches 271. .309 of consensus"   |
| repeat_region | 51830. .52172<br>/note="THE1B repeat: matches 1. .364 of consensus"      |
| repeat_region | 52173. .52221<br>/note="MER74A repeat: matches 221. .271 of consensus"   |
| repeat_region | 52710. .53396<br>/note="L1MB7 repeat: matches 5451. .6171 of consensus"  |
| repeat_region | 53890. .53996  |

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repeat_region      /note="MIR repeat: matches 35. .152 of consensus"
                    54259. .54296
repeat_region      /note="19 copies 2 mer tt 84% conserved"
                    54299. .55519
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Query Match          66.1%; Score 2841.8; DB 9; Length 183337;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2854; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy      1490 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 1549
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Qy      1550 AATACAGCTCATCTTGAAAGAAGAACTATTTCACTGTATTTTCATTTTCTTTATATTGGACC 1609
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Db      72710 AATACAGCTCATCTTGAAAGAAGAACTATTTCACTGTATTTTCATTTTCTTTATATTGGACC 72651

Qy      1610 GAAGTCATTAAAAACAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA 1669
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Db      72650 GAAGTCATTAAAAACAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA 72591

Qy      1670 CAGCACACTATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT 1729
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Db      72590 CAGCACACTATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT 72531

Qy      1730 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGA 1789
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Qy 2810 AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT 2869  
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 Db 71450 AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT 71391

Qy 2870 AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCT 2929  
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 Db 71390 AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCT 71331

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 Db 70251 TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTGGTTGCCTAAAGTGGCTATA 70192  
 QY 4070 GTTACTGATTTTTTATTATGTAAGCAAACCAATAAAATTTAAGTTTTTTTAAACAACTA 4129  
 Db 70191 GTTACTGATTTTTTATTATGTAAGCAAACCAATAAAATTTAAGTTTTTTTAAACAACTA 70132  
 QY 4130 CCTTATTTTTCTACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA 4189  
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 Db 70011 GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 69975

# RESULT 9

AC144750/c

LOCUS AC144750 201093 bp DNA linear HTG 04-JUN-2003

DEFINITION Pan troglodytes clone CH251-517B22, WORKING DRAFT SEQUENCE, 3 ordered pieces.

ACCESSION AC144750

VERSION AC144750.2 GI:31376422

KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 201093)

AUTHORS Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K., Chu,G., Coleman,B., Coleman,H., Engle,J., Granite,S., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B., Idol,J.R., Karlins,E., Kwong,P., Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B., McDowell,J., Paguirigan,C., Pearson,R., Portnoy,M.E., Prasad,A., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Shah,K., Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.

TITLE NISC Comparative Sequencing Initiative

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 201093)  
 AUTHORS Green,E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-MAY-2003) NIH Intramural Sequencing Center, 8717  
 Grovemont Circle, Gaithersburg, MD 20877, USA  
 REFERENCE 3 (bases 1 to 201093)  
 AUTHORS Green,E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-JUN-2003) NIH Intramural Sequencing Center, 8717  
 Grovemont Circle, Gaithersburg, MD 20877, USA  
 COMMENT On Jun 4, 2003 this sequence version replaced gi:30725907.

----- Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: <http://www.nisc.nih.gov>  
 Contact: [nisc\\_zoo@nhgri.nih.gov](mailto:nisc_zoo@nhgri.nih.gov)  
 ----- Project Information  
 Center project name: esg  
 Center clone name: 517B22

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 200649 bases at least Q40  
 Consensus quality: 200775 bases at least Q30  
 Consensus quality: 200836 bases at least Q20  
 Insert size: 165000; agarose-fp  
 Insert size: 200893; sum-of-contigs  
 Quality coverage: 13.47x in Q20 bases; agarose-fp  
 Quality coverage: 11.07x in Q20 bases; sum-of-contigs

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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 3 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submittor.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 \* 1 107546: contig of 107546 bp in length  
 \* 107547 107646: gap of unknown length  
 \* 107647 153000: contig of 45354 bp in length  
 \* 153001 153100: gap of unknown length

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* 153101 201093: contig of 47993 bp in length.
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                    /note="clone overlaps with GenBank Accession Number
                    AC144499 clone RP43-108D19 (center project name esf)"
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# ORIGIN

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Best Local Similarity 99.2%;  Pred. No. 0;
Matches 2838;  Conservative 0;  Mismatches 16;  Indels 6;  Gaps 3;

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| Qy | 3347  | TTTATAAATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCT | 3406  |
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| Db | 67799 | TTTATAAATCACCCACAACTTGTTTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCT  | 67740 |
| Qy | 3407  | GTTATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTT | 3466  |
|    |       |  |       |
| Db | 67739 | GTTATCATAGAAGACATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTT | 67680 |
| Qy | 3467  | TCACAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGT  | 3526  |
|    |       |  |       |
| Db | 67679 | TCACAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGT  | 67620 |
| Qy | 3527  | ACTGAATTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATT  | 3586  |
|    |       |  |       |
| Db | 67619 | ACTGAATTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATT  | 67560 |

Qy 3587 ATCTTGCCAAATTTTGAAGTACACACAAAAGCATACTTGCATTATTTATAATAAAATT 3646  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 67559 ATCTTGCCAAATTTTGAAGTACACACAAAAGCATACTTGCATTATTTATAATAAAATT 67500

Qy 3647 GCATTCAGTGGCTTTTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAA 3706  
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 Db 67499 GCATTCAGTGGCTTTTT-AAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAA 67441

Qy 3707 GAAACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCA 3766  
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 Db 67440 GAAACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCA 67381

Qy 3767 ACTTCAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGT 3826  
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 Db 67380 ACTTCAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGT 67321

Qy 3827 TAACATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTAT 3886  
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 Db 67320 TAACATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTAT 67261

Qy 3887 TATCCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATG 3946  
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 Db 67260 TATCCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATG 67201

Qy 3947 GCCAAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTG 4006  
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 Db 67200 GCCAAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTG 67141

Qy 4007 TAATATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCT 4066  
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 Db 67140 TAATATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCT 67081

Qy 4067 ATAGTTACTGATTTTTTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACAA 4126  
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 Db 67080 ATAGTTACTGATTTTTTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACAA 67021

Qy 4127 CTACCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAG 4186  
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 Db 67020 CTACCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAG 66961

Qy 4187 AAATATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTAT 4246  
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 Db 66960 AAATATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTAT 66901

Qy 4247 GAAGTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 4286  
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 Db 66900 GAAGTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 66861

RESULT 10

G06417

LOCUS G06417 2720 bp DNA linear STS 19-OCT-1995

DEFINITION human STS WI-7149, sequence tagged site.

ACCESSION G06417

VERSION G06417.1 GI:859662

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2720)

AUTHORS Hudson, T.

TITLE Whitehead Institute/MIT Center for Genome Research; Physically  
 Mapped ESTs

JOURNAL Unpublished (1995)

COMMENT

Contact: Thomas Hudson  
 Whitehead Institute/MIT Center for Genome Research  
 Whitehead Institute for Biomedical Research  
 9 Cambridge Center, Cambridge MA 02142 USA  
 Tel: 617 252 1900  
 Fax: 617 252 1902  
 Email: thudson@genome.wi.mit.edu

Primer A: ATGGAGAGATGCCAGTGACC

Primer B: TAGGCAGGAACGCACAAAG

STS size: 331

PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pM

dNTPs: each 4 nM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCL: 10 mM

pH: 9.3

Prepared with primer pairs derived from D90402 -- Unigene.

FEATURES

Location/Qualifiers

source 1. .2720  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /map="710\_D\_4; 788\_D\_1; 795\_F\_4; 921\_F\_2; 940\_G\_8;  
 969\_D\_1"

STS 1005. .1335

primer\_bind 1005. .1024

primer\_bind complement(1317. .1335)

ORIGIN

Query Match 60.7%; Score 2610; DB 11; Length 2720;  
 Best Local Similarity 96.0%; Pred. No. 0;  
 Matches 2610; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

|    |     |   |      |
|----|-----|---|------|
| Qy |     | 1567 AAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAAAACAAA | 1626 |
|    |     |   |      |
| Db | 1   | AAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTNNNNNNNNN      | 60   |
|    |     |   |      |
| Qy |     | 1627 ATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTATTAAAAT   | 1686 |
|    |     |   |      |
| Db | 61  | NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTATGTATTTGCACAGCACACTATTAAAAT        | 120  |
|    |     |   |      |
| Qy |     | 1687 ATTAAGTGTAATTATTTTAACTCAGCTACATATGACATTTTATGAGCTGTTTACGG       | 1746 |
|    |     |   |      |
| Db | 121 | ATTAAGTGTAATTATTTTAACTCAGCTACATATGACATTTTATGAGCTGTTTACGG            | 180  |
|    |     |   |      |
| Qy |     | 1747 CATGGAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAATTTTTTA     | 1806 |
|    |     |   |      |
| Db | 181 | CATGGAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAATTTTTTA          | 240  |
|    |     |   |      |
| Qy |     | 1807 CAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACTTAGGCT   | 1866 |
|    |     |   |      |
| Db | 241 | CAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACTTAGGCT        | 300  |
|    |     |   |      |
| Qy |     | 1867 TAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTAAATCAA   | 1926 |
|    |     |   |      |
| Db | 301 | TAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTAAATCAA        | 360  |
|    |     |   |      |
| Qy |     | 1927 TGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGA ACTTTTTAAATGAAGCTT | 1986 |
|    |     |   |      |
| Db | 361 | TGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGA ACTTTTTAAATGAAGCTT      | 420  |
|    |     |   |      |
| Qy |     | 1987 AAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATATTATCAC  | 2046 |
|    |     |   |      |
| Db | 421 | AAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATATTATCAC       | 480  |
|    |     |   |      |
| Qy |     | 2047 ACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCATTTTTTCG  | 2106 |
|    |     |   |      |
| Db | 481 | ACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCATTTTTTCG       | 540  |
|    |     |   |      |
| Qy |     | 2107 GACACTGGAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGTTTTTGA    | 2166 |
|    |     |   |      |
| Db | 541 | GACACTGGAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGTTTTTGA         | 600  |
|    |     |   |      |
| Qy |     | 2167 AAATCATTACACTTTTCACTAGAAGCCCCAACCTCAGCATTTCTGCAATATGTAACCAACAT | 2226 |
|    |     |   |      |
| Db | 601 | AAATCATTACACTTTTCACTAGAAGCCCCAACCTCAGCATTTCTGCAATATGTAACCAACAT      | 660  |
|    |     |   |      |
| Qy |     | 2227 GTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAATATAAT   | 2286 |
|    |     |   |      |
| Db | 661 | GTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAATATAAT        | 720  |
|    |     |   |      |
| Qy |     | 2287 ACTTTTAAAAGAAAATTATTACATCCTTTACATTCA GTTAAGATCAAACCTCACAAAGA   | 2346 |
|    |     |   |      |
| Db | 721 | ACTTTTAAAAGAAAATTATTACATCCTTTACATTCA GTTAAGATCAAACCTCACAAAGA        | 780  |
|    |     |   |      |
| Qy |     | 2347 GAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTACATACC     | 2406 |
|    |     |   |      |
| Db | 781 | GAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTACATACC          | 840  |
|    |     |   |      |
| Qy |     | 2407 CTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTTTCACTA  | 2466 |



|    |      |  |   |      |
|----|------|--|---|------|
| Db | 841  |  | CTGTGAAGACAATACTATCTACAATTTTTCAGGATTATTAAAATCTTCTTTTTTCACTA   | 900  |
| Qy | 2467 |  | TCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACACTGCAT  | 2526 |
| Db | 901  |  | TCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACACTGCAT  | 960  |
| Qy | 2527 |  | GTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGATGCCAGT  | 2586 |
| Db | 961  |  | GTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGATGCCAGT  | 1020 |
| Qy | 2587 |  | GACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGGGCAGGT  | 2646 |
| Db | 1021 |  | GACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGGGCAGGT  | 1080 |
| Qy | 2647 |  | AGCACCCCTCTCTCAGGATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAATGCTATA  | 2706 |
| Db | 1081 |  | AGCACCCCTCTCTCAGGATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAATGCTATA  | 1140 |
| Qy | 2707 |  | GTTAAAATACTATTTTTCAAATCATAAGATTAGTACATTTAACAGCTACCTGTAAAGC    | 2766 |
| Db | 1141 |  | GTTAAAATACTATTTTTCAAATCATAAGATTAGTACATTTAACAGCTACCTGTAAAGC    | 1200 |
| Qy | 2767 |  | TTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTGACATGG  | 2826 |
| Db | 1201 |  | TTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTGACATGG  | 1260 |
| Qy | 2827 |  | TGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTTAGCTTT   | 2886 |
| Db | 1261 |  | TGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTTAGCTTT   | 1320 |
| Qy | 2887 |  | GTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTTGGGATG  | 2946 |
| Db | 1321 |  | GTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTTGGGATG  | 1380 |
| Qy | 2947 |  | AGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTGGGGTTG  | 3006 |
| Db | 1381 |  | AGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTGGGGTTG  | 1440 |
| Qy | 3007 |  | GAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTATTGCCTCGTCAC  | 3066 |
| Db | 1441 |  | GAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTATTGCCTCGTCAC  | 1500 |
| Qy | 3067 |  | ATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCAGAGTGA   | 3126 |
| Db | 1501 |  | ATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCAGAGTGA   | 1560 |
| Qy | 3127 |  | CTTTCGAAATAAATTTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAAATTTT | 3186 |
| Db | 1561 |  | CTTTCGAAATAAATTTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAAATTTT | 1620 |
| Qy | 3187 |  | ACTTTGTTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATGTTGTTT   | 3246 |
| Db | 1621 |  | ACTTTGTTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATGTTGTTT   | 1680 |
| Qy | 3247 |  | TCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCAGAAAGA   | 3306 |
|    |      |  |   |      |

Db 1681 TCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCAGAAAGA 1740

Qy 3307 AAGAGCAATAATAATTAATTACACACCCATATGGATTCTATTTATAAATCACCCACAAAC 3366  
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Db 1741 AAGAGCAATAATAATTAATTACACACCCATATGGATTCTATTTATAAATCACCCACAAAC 1800

Qy 3367 TTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGTCATTTT 3426  
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Db 1801 TTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGTCATTTT 1860

Qy 3427 AGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAATATATT 3486  
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Db 1861 AGACTCTCAATTTTAAATTAATTTTGAATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1920

Qy 3487 TAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACATCCTGA 3546  
 |||

Db 1921 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTACCATGTACTGAATTTTACATCCTGA 1980

Qy 3547 TACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTTTGAAAC 3606  
 |||

Db 1981 TACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTTTGAAAC 2040

Qy 3607 TACACACAAAAGCATACTTGCATTATTTATAATAAAATTCATTTCAGTGGCTTTTTTAAA 3666  
 |||

Db 2041 TACACACAAAAGCATACTTGCATTATTTATAATAAAATTCATTTCAGTGGCTTTTTNNN 2100

Qy 3667 AAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAATTTCTTT 3726  
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Db 2101 NNNNNTGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAATTTCTTT 2160

Qy 3727 ACATACTCAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAACATGTTTCCTA 3786  
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Db 2161 ACATACTCAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAACATGTTTCCTA 2220

Qy 3787 GTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTACAGCTC 3846  
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Db 2221 GTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTACAGCTC 2280

Qy 3847 AAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAATGTGGAT 3906  
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Db 2281 AAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAATGTGGAT 2340

Qy 3907 GTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACAGTTTAT 3966  
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Db 2341 GTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACAGTTTAT 2400

Qy 3967 AGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGTAAAAA 4026  
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Db 2401 AGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGTAAAAA 2460

Qy 4027 TTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTTTTTATT 4086  
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Db 2461 TTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTTTTTATT 2520

Qy 4087 ATGTAAGCAAAACCAATAAAAAATTAAGTTTTTTTAACTACCTTATTTTCACTGTA 4146  
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Db 2521 ATGTAAGCAAAACCAATAAAAAATTAAGTTTTTTTAACTACCTTATTTTCACTGTA 2580

QY 4147 CAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGACAAGTG 4206  
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 Db 2581 CAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGACAAGTG 2640  
 QY 4207 GACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATTAAAATG 4266  
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 Db 2641 GACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATTAAAATG 2700  
 QY 4267 CCACATTTCTGGTCTCTGGG 4286  
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 Db 2701 CCACATTTCTGGTCTCTGGG 2720

RESULT 11

AC130785/c

LOCUS AC130785 169751 bp DNA linear HTG 29-AUG-2002

DEFINITION Papio anubis clone RP41-325P5, WORKING DRAFT SEQUENCE.

ACCESSION AC130785

VERSION AC130785.1 GI:22218455

KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.

SOURCE Papio anubis (olive baboon)

ORGANISM Papio anubis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 Cercopithecinae; Papio.

REFERENCE 1 (bases 1 to 169751)

AUTHORS Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,  
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,  
 Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,  
 Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E.,  
 Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,  
 Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D.,  
 McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R.,  
 Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schueler, M.G., Sison, C.,  
 Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,  
 Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

TITLE NISC Comparative Sequencing Initiative

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 169751)

AUTHORS Green, E.D.

TITLE Direct Submission

JOURNAL Submitted (14-AUG-2002) NIH Intramural Sequencing Center, 8717  
 Grovemont Circle, Gaithersburg, MD 20877, USA

REFERENCE 3 (bases 1 to 169751)

AUTHORS Green, E.D.

TITLE Direct Submission

JOURNAL Submitted (29-AUG-2002) NIH Intramural Sequencing Center, 8717  
 Grovemont Circle, Gaithersburg, MD 20877, USA

COMMENT

----- Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: <http://www.nisc.nih.gov>  
 Contact: [nisc\\_zoo@nhgri.nih.gov](mailto:nisc_zoo@nhgri.nih.gov)  
 ----- Project Information  
 Center project name: deh  
 Center clone name: 325P05

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 169735 bases at least Q40  
 Consensus quality: 169747 bases at least Q30  
 Consensus quality: 169749 bases at least Q20  
 Insert size: 138000; agarose-fp  
 Insert size: 169751; sum-of-contigs  
 Quality coverage: 10.99x in Q20 bases; agarose-fp  
 Quality coverage: 8.94x in Q20 bases; sum-of-contigs

-----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 1 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.

FEATURES

source

1 169751: contig of 169751 bp in length.  
 Location/Qualifiers

1. .169751  
 /organism="Papio anubis"  
 /mol\_type="genomic DNA"  
 /sub\_species="anubis"  
 /db\_xref="taxon:9555"  
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 /clone\_lib="RP41"

misc\_feature

1. .169751  
 /note="assembly\_fragment  
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 vector\_side:left  
 clone\_end:Sp6  
 vector\_side:right"

misc\_feature

1. .63149  
 /note="clone overlaps with GenBank Accession Number  
 AC129069 clone RP41-240D13 (center project name deg)"

ORIGIN

Query Match 59.3%; Score 2550; DB 2; Length 169751;  
 Best Local Similarity 94.8%; Pred. No. 0;  
 Matches 2717; Conservative 0; Mismatches 130; Indels 19; Gaps 7;

Qy 1430 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 1489  
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 Db 29218 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 29159

Qy 1490 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATA 1549  
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 Db 29158 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATA 29099

Qy 1550 AATACAGCTCATCTTGAAAGAAGAACTATTTACTGTATTTTCTTTTATATTGGACC 1609  
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 Db 29098 AATACAGCTCATCTTGAAAGAAGAACTATTTACTGTATTTTCTTTTATATTGGACC 29039

Qy 1610 GAAGTCATTAAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA 1669  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 29038 GAAGTCATTAAAAACAAAATGAAACATTTGTCAAACAAAACAAAAAACTATGTATTTGCA 28979

Qy 1670 CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATT 1729  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 28978 CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACTCATAGCTACATATGACATT 28919

Qy 1730 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA 1789  
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 Db 28918 TTATGAGCTGTTTACAGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCATTGTGA 28859

Qy 1790 AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATT 1849  
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Qy 1850 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG 1909  
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Qy 1910 ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA 1969  
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Qy 1970 ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTT 2029  
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 Db 28686 ACTTTTAAATGAAGCTTAAATTACCCAATTTGAAATTTTAAAATCCTTTAAAAGAACCTT 28627

Qy 2030 TCAATTAATATTATCACACT-ATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTT 2088  
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Qy 2089 TAGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAA 2148  
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Qy 2149 GAGCAAGGCTGTTTTTGAAAATCATTACA---CTTTCCTAGTAAGCCCAAACCTCAGCAT 2205  
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 Db 28506 GAACAAGGCTGTTTTTGAAAATCATTACACTCCTTTCCTAGTAAGCCCAAACCTCAGCAT 28447

Qy 2206 TCTGCAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGC 2265  
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QY 2266 CAGCTGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGT 2325  
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 Db 28386 CAGCCAAATCTAAAATATAATACTTTTAAAAAGAAAATTATTACACCCTTTACATTTCAGA 28327  
 QY 2326 TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTT 2385  
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 QY 2386 TGAATCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTAT 2445  
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 Db 28266 TGAATCTGCCATTACACAGCCTGTGAAGAAAATACTATCTACAAATTTTTTCAGGATTAT 28207  
 QY 2446 TAAATCTTCTTTTTTCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAAT 2505  
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 Db 28206 TAAATCTTCTTCTTTCACTATTGTAGCTTAACTCTGTTTGGTTTTGTCATCCGTAAAT 28147  
 QY 2506 ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT 2565  
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 QY 2746 TTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAAT 2805  
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 QY 2806 AGAAAAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCAAACCTGCTTTTTGAGA 2865  
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 QY 2866 CCGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGT 2925  
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 QY 2926 GCCTTAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAG 2985  
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 Db 27726 GCCTTAGAATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAG 27667  
 QY 2986 AGAGGAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAA 3045  
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 QY 3046 CGTTCGTCATTGCCTCGTCACATCAATGCAAAGGTCCTGATTTTGTCCAGCAAACAC 3105  
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 Db 27606 CGTTCGTCATTGCCTCGTCACATCAATGCAAAGGTCCTGATTTTGTCCAGCAAACAC 27547  
 QY 3106 AGTGCAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTC 3165

|    |       |  |       |
|----|-------|--|-------|
| Db | 27546 | AGTGCAATGTTCTCAGAGTGACTTTAGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTC   | 27487 |
| Qy | 3166  | TTAAAATATGCCCAAATTTTTACTTTGTTTTCTTTTAAATAGGCTGGGCCACATGTTGGA   | 3225  |
| Db | 27486 | TTAAAATATGCCCAAATTTTTACTTTTTTTTCTTTTAGTAAACTGGGCCACATGTTGGA    | 27427 |
| Qy | 3226  | AATAAGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAAC   | 3285  |
| Db | 27426 | AATAAGCTAGTAATGTTGTTTTCTGTCAATATCGAATGTGATGGTGCAGTAAACCAAAAC   | 27367 |
| Qy | 3286  | CCAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCT   | 3345  |
| Db | 27366 | CCAACAATGTGGCCAGAAAGAAAGAGCAATAATGATTAATTCACATGCCATGTGGATTCT   | 27307 |
| Qy | 3346  | ATTTATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCC | 3405  |
| Db | 27306 | ATTTATAAATCACCCACAAACTTGTTTTTTAATTTTCATCCCAATCATTTTTTCAGAGGCC  | 27247 |
| Qy | 3406  | TGTTATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATT    | 3465  |
| Db | 27246 | TGTTATCATAGAAGACATTTTAGACTTGCAATTTTAAATTAATTTGAATCACTAATATT    | 27187 |
| Qy | 3466  | TTCACAGTTTATTAATATA-TTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCAT   | 3524  |
| Db | 27186 | TTCACAGTTTATTAATATATTTTTATTCTATTTAAATTTTAGATTATTTTTATTACCAT    | 27127 |
| Qy | 3525  | GTAAGTGAATTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAA   | 3584  |
| Db | 27126 | GTAAGTGAATTTTATATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTGTAA   | 27067 |
| Qy | 3585  | TTATCTTGCCAAATTTTGAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAA   | 3644  |
| Db | 27066 | TTATCTTACCAAATTTTGAACTGCACACAAAAAGCATACTTGCAATTATTTATAATAAAA   | 27007 |
| Qy | 3645  | TTGCATTCAAGTGGCTTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGT   | 3704  |
| Db | 27006 | TTGCATTCAAGTGGCTTTTT-AAAAAATGTTTGATTCAAAATTTAACATACTGATAAGT    | 26948 |
| Qy | 3705  | AAGAAACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTT    | 3764  |
| Db | 26947 | AAGAAACAATAATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATTATT    | 26888 |
| Qy | 3765  | CAACTTCAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATT    | 3824  |
| Db | 26887 | TAAGTTCCAAACATGTTTCCTAGTATTAAGAACTTTAATATAGCAACAGACAAAATTATT   | 26828 |
| Qy | 3825  | GTTAACATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTT    | 3884  |
| Db | 26827 | GTTAACATGAATGTTACAGCTCAGAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTT   | 26768 |
| Qy | 3885  | ATTATCCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATA   | 3944  |
| Db | 26767 | ATTATCCACTGCTAATGTGGATATATGTTCAAACACCTTTTAGTATTGATAGCTTACATA   | 26708 |
| Qy | 3945  | TGGCCAAAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAG   | 4004  |

Db 26707 TGGCCAAAGGAATACAGTTTATAGTGAAACATGGGTATACTGTAGCTAACTTTATAAAAC 26648

Qy 4005 TGTAATATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGG 4064  
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Db 26647 TGTAATATAACAATGTAAAAAATTATATACCTGGGGGATTTTTTGGTTGCTTAAAGTGG 26588

Qy 4065 CTATAGTTACTGA-TTTTTTATTATGTAAGCAAACCAATAAA----AATTTAAGTTTTT 4119  
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Db 26587 CTATAGTCACTGATTTTTTTATTATGTAAGCAAACCAATAAACTTTAGGTTGTGTTTTT 26528

Qy 4120 TTAACAACTACCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGT 4179  
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Db 26527 TTAACAACTAGCTTATTTTTTCATTGTACAGGCACTAATTCATTAAATACTAATTGACTGT 26468

Qy 4180 TTAAAAGAAATATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAG 4239  
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Db 26467 TTAAAGGAAATATAAATGTGACAAGTGGACACTATTTATGTTAAATATACAATCATCAAG 26408

Qy 4240 CAAGTATGAAGTTATTCAATTAAAATGCCACATTTCTGGTCTCTGG 4285  
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# RESULT 12

AC129069/c

LOCUS AC129069 185870 bp DNA linear HTG 19-SEP-2002

DEFINITION Papio anubis clone RP41-240D13, WORKING DRAFT SEQUENCE.

ACCESSION AC129069

VERSION AC129069.2 GI:23196382

KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.

SOURCE Papio anubis (olive baboon)

ORGANISM Papio anubis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 Cercopithecinae; Papio.

REFERENCE 1 (bases 1 to 185870)

AUTHORS Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,  
 Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,  
 Cariaga,K., Coleman,B., Dietrich,N.L., Granite,S., Guan,X.,  
 Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R.,  
 Karlins,E., Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L.,  
 Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B.,  
 Mastrian,S.D., McCloskey,J.C., McDowell,J., Paguirigan,C.,  
 Pearson,R., Portnoy,M.E., Prasad,A., Reddix-Dugue,N.,  
 Schueler,M.G., Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J.,  
 Touchman,J.W., Vogt,J.L., Walker,M., Wetherby,K.D., Wiggins,L.,  
 Young,A., Zhang,L.-H. and Green,E.D.

TITLE NISC Comparative Sequencing Initiative

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 185870)

AUTHORS Green,E.D.

TITLE Direct Submission

JOURNAL Submitted (25-JUL-2002) NIH Intramural Sequencing Center, 8717

Grovemont Circle, Gaithersburg, MD 20877, USA

REFERENCE 3 (bases 1 to 185870)

AUTHORS Green,E.D.

TITLE Direct Submission



JOURNAL Submitted (19-SEP-2002) NIH Intramural Sequencing Center, 8717  
Grovemont Circle, Gaithersburg, MD 20877, USA  
COMMENT On Sep 19, 2002 this sequence version replaced gi:21955004.

----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: <http://www.nisc.nih.gov>  
Contact: [nisc\\_zoo@nhgri.nih.gov](mailto:nisc_zoo@nhgri.nih.gov)

----- Project Information  
Center project name: deg  
Center clone name: 240D13

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics  
Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 184076 bases at least Q40  
Consensus quality: 185363 bases at least Q30  
Consensus quality: 185733 bases at least Q20  
Insert size: 152000; agarose-fp  
Insert size: 185870; sum-of-contigs  
Quality coverage: 7.20x in Q20 bases; agarose-fp  
Quality coverage: 5.89x in Q20 bases; sum-of-contigs

-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 1 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submittor.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 185870: contig of 185870 bp in length.

FEATURES

source

Location/Qualifiers  
1. .185870  
/organism="Papio anubis"  
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/db\_xref="taxon:9555"  
/clone="RP41-240D13"  
/clone\_lib="RP41"

misc\_feature

1. .185870  
/note="assembly\_fragment  
clone\_end:T7  
vector\_side:left

missing approximately 55 bases, including Sp6 clone end,  
on 3' end of insert"  
misc\_feature 121812. .185870  
/note="clone overlaps with GenBank Accession Number  
AC130785 clone RP41-325P5 (center project name deh)"

ORIGIN

Query Match 59.3%; Score 2550; DB 2; Length 185870;  
Best Local Similarity 94.8%; Pred. No. 0;  
Matches 2717; Conservative 0; Mismatches 130; Indels 19; Gaps 7;

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Qy      1430 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 1489
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Db      151685 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC
151626

Qy      1490 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 1549
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| 151094 |        |   |      |  |
| Qy     | 2030   | TCAATTAATATTATCACACT-ATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTT  | 2088 |  |
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| Qy     | 2089   | TAGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAA | 2148 |  |
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| Db     | 151033 | TAGTTGCTGTATTTTTTGACACTAGAAACATTTAAATGATCAGGAGGGAGTAACTGAAA   |      |  |
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| Qy     | 2149   | GAGCAAGGCTGTTTTTGAAAATCATTACA---CTTTCACTAGAAGCCCAAACCTCAGCAT  | 2205 |  |
|        |        |   |      |  |
| Db     | 150973 | GAACAAGGCTGTTTTTGAAAATCATTACACTCCTTTCACTAGAAGCCCAAACCTCAGCAT  |      |  |
| 150914 |        |   |      |  |
| Qy     | 2206   | TCTGCAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGC  | 2265 |  |
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| 150854 |        |   |      |  |
| Qy     | 2266   | CAGCTGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAGT  | 2325 |  |
|        |        |   |      |  |
| Db     | 150853 | CAGCCAAATCTAAAATATAATACTTTTAAAAAGAAAATTATTACACCCTTTACATTCAGA  |      |  |
| 150794 |        |   |      |  |
| Qy     | 2326   | TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCCAAAGACTTTTTT | 2385 |  |
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| Db     | 150793 | TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTGCCCAAAGACTTCTT    |      |  |
| 150734 |        |   |      |  |
| Qy     | 2386   | TGAATCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTAT   | 2445 |  |
|        |        |   |      |  |
| Db     | 150733 | TGAATCTGCCATTACACAGCCTGTGAAGAAAATACTATCTACAAATTTTTTCAGGATTAT  |      |  |
| 150674 |        |   |      |  |
| Qy     | 2446   | TAAAATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAAT  | 2505 |  |
|        |        |   |      |  |
| Db     | 150673 | TAAAATCTTCTTCTTTCACTATTGTAGCTTAAACTCTGTTTGGTTTTGTCATCCGTAAAT  |      |  |
| 150614 |        |   |      |  |
| Qy     | 2506   | ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT  | 2565 |  |
|        |        |   |      |  |
| Db     | 150613 | ACTTAGCTACATACACTGCATGTAGACGATTAAACGAGGGCGGGCCCTGTGTTTCATAGTT |      |  |
| 150554 |        |   |      |  |
| Qy     | 2566   | TTACGATGGAGAGATGCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGT   | 2625 |  |
|        |        |   |      |  |
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| 150494 |        |   |      |  |
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Db 150193 GCCTTAGAATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAG  
 150134

Qy 2986 AGAGGAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATCCCATTCTTAGCCTAA 3045  
 |||||

Db 150133 AGAGGAAATGAGGTGGGGTGAGAGGAAACTCATGGGGACAGATCCCATTCTTAGCCTAA  
 150074

Qy 3046 CGTTCGTCATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAACAC 3105  
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Db 150073 CGTTCGTCATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAACAC  
 150014

Qy 3106 AGTGCAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTC 3165  
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Db 150013 AGTGCAATGTTCTCAGAGTGACTTTAGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTC  
 149954

Qy 3166 TTAAATATGCCCAAATTTTTACTTTGTTTTCTTTTAAATAGGCTGGGCCACATGTTGGA 3225  
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Db 149953 TTAAATATGCCCAAATTTTTACTTTTTTTCTTTTAGTAACTGGGCCACATGTTGGA  
 149894

Qy 3226 AATAAGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAC 3285  
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Db 149893 AATAAGCTAGTAATGTTGTTTTCTGTCAATATCGAATGTGATGGTGCAGTAAACCAAAC  
 149834

Qy 3286 CCAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCT 3345  
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Db 149833 CCAACAATGTGGCCAGAAAGAAAGAGCAATAATGATTAATTCACATGCCATGTGGATTCT  
 149774

Qy 3346 ATTTATAAATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCC 3405  
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 Db 149773 ATTTATAAATCACCCACAACTTGTTTTTTAATTTTCATCCCAATCATTTTTTCAGAGGCC  
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Qy 3406 TGTTATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATT 3465  
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 Db 149713 TGTTATCATAGAAGACATTTTAGACTTGCAATTTTAAATTAATTTTGAATCACTAATATT  
 149654

Qy 3466 TTCACAGTTTATTAATATA-TTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCAT 3524  
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 Db 149653 TTCACAGTTTATTAATATATTTTTATTTCTATTTAAATTTTAGATTATTTTTATTACCAT  
 149594

Qy 3525 GTACTGAATTTTTACATCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAA 3584  
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 149534

Qy 3585 TTATCTTGCCAAATTTTGAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAAA 3644  
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 Db 149533 TTATCTTACCAAATTTTGAACTGCACACAAAAAGCATACTTGCAATTATTTATAATAAAAA  
 149474

Qy 3645 TTGCATTTCAGTGGCTTTTTTAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGT 3704  
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 Db 149473 TTGCATTTCAGTGGCTTTTT-AAAAAATGTTTGATTCAAAATTTAACATACTGATAAGT  
 149415

Qy 3705 AAGAAACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTT 3764  
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 Db 149414 AAGAAACAATAATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATTATT  
 149355

Qy 3765 CAACTTCAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATT 3824  
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 Db 149354 TAACTTCAAACATGTTTCCTAGTATTAAGAATTTAATATAGCAACAGACAAAATTATT  
 149295

Qy 3825 GTTAACATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTT 3884  
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 Db 149294 GTTAACATGAATGTTACAGCTCAGAAGATTTATAAAAGATTTTAACTATTTTCTCCCTT  
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Qy 3885 ATTATCCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATA 3944  
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 Db 149234 ATTATCCACTGCTAATGTGGATATATGTTCAAACACCTTTTAGTATTGATAGCTTACATA  
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Qy 3945 TGGCCAAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAG 4004  
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 Db 149174 TGGCCAAAGGAATACAGTTTATAGTGAAACATGGGTATACTGTAGCTAACTTTATAAAAC  
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Qy 4005 TGTAATATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGG 4064

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Db 149114 TGTAATATAACAATGTAAAAAATTATATACCTGGGGGGATTTTTTGGTTGCTTAAAGTGG
149055

Qy 4065 CTATAGTTACTGA-TTTTTTATTATGTAAGCAAAACCAATAAA----AATTTAAGTTTTT 4119
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Db 149054 CTATAGTCACTGATTTTTTTATTATGTAAGCAAAACCAATAAACTTTAGGTTGTGTTTTT
148995

Qy 4120 TTAACAACCTACCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGT 4179
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Db 148994 TTAACAACCTAGCTTATTTTTTCATTGTACAGGCACTAATTCATTAAATACTAATTGACTGT
148935

Qy 4180 TTAAGGAAATATAAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAG 4239
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Db 148934 TTAAGGAAATATAAAATGTGACAAGTGGACACTATTTATGTTAAATATACAATCATCAAG
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Qy 4240 CAAGTATGAAGTTATTCAATTAAAATGCCACATTTCTGGTCTCTGG 4285
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Db 148874 GAAGTATGAAGTTATTCAATTAAAATGCCACATTTCTGGTCTCTGG 148829

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# RESULT 13

AR165435

LOCUS AR165435 1873 bp DNA linear PAT 17-OCT-2001

DEFINITION Sequence 13 from patent US 6280931.

ACCESSION AR165435

VERSION AR165435.1 GI:16240327

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1873)

AUTHORS Sakamoto,A. and Hanaoka,F.

TITLE Method for specifically amplifying a dystroglycan,  
.alpha.-sarcoglycan, or endothelin Breceptor cDNA of an extremely  
small

JOURNAL Patent: US 6280931-A 13 28-AUG-2001;

FEATURES Location/Qualifiers

source 1. .1873

/organism="unknown"

/mol\_type="unassigned DNA"

## ORIGIN

Query Match 39.3%; Score 1691.8; DB 6; Length 1873;  
Best Local Similarity 99.6%; Pred. No. 5.5e-293;  
Matches 1696; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237
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Db 171 TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 230

Qy 238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297
|||||

Db 231 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 290

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|    |      |  |      |
|----|------|--|------|
| Qy | 298  | CTGTGCGGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG   | 357  |
|    |      |  |      |
| Db | 291  | CTGTGCGGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG   | 350  |
| Qy | 358  | CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC   | 417  |
|    |      |  |      |
| Db | 351  | CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC   | 410  |
| Qy | 418  | AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT  | 477  |
|    |      |  |      |
| Db | 411  | AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT  | 470  |
| Qy | 478  | CCGCCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC    | 537  |
|    |      |  |      |
| Db | 471  | CCGCCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC    | 530  |
| Qy | 538  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCC | 597  |
|    |      |  |      |
| Db | 531  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCC | 590  |
| Qy | 598  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 657  |
|    |      |  |      |
| Db | 591  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 650  |
| Qy | 658  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 717  |
|    |      |  |      |
| Db | 651  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 710  |
| Qy | 718  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA  | 777  |
|    |      |  |      |
| Db | 711  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA  | 770  |
| Qy | 778  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 837  |
|    |      |  |      |
| Db | 771  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 830  |
| Qy | 838  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTCCAAAATGGACAGCAGTA    | 897  |
|    |      |  |      |
| Db | 831  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTCCAAAATGGACAGCAGTA    | 890  |
| Qy | 898  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 957  |
|    |      |  |      |
| Db | 891  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 950  |
| Qy | 958  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1017 |
|    |      |  |      |
| Db | 951  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1010 |
| Qy | 1018 | CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC  | 1077 |
|    |      |  |      |
| Db | 1011 | CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTATTTCAGTTTC  | 1070 |
| Qy | 1078 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATG   | 1137 |
|    |      |  |      |
| Db | 1071 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATG   | 1130 |

Qy 1138 TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA 1197  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1131 TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA 1190  
 Qy 1198 GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC 1257  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1191 GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC 1250  
 Qy 1258 CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT 1317  
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 Db 1251 CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT 1310  
 Qy 1318 TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC 1377  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1311 TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC 1370  
 Qy 1378 ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAAGATTCAAAAAGCTTTAAGTCATGC 1437  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1371 ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAAGATTCAAAAAGCTTTAAGTCATGC 1430  
 Qy 1438 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC 1497  
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 Db 1431 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC 1490  
 Qy 1498 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGC 1557  
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 Db 1491 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGC 1550  
 Qy 1558 TCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT 1617  
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 Db 1551 TCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT 1610  
 Qy 1618 TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC 1677  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1611 TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC 1670  
 Qy 1678 TATTAAATATTAAGTGAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC 1737  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1671 TATTAAATATTAAGTGAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC 1730  
 Qy 1738 TGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1797  
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 Db 1731 TGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1790  
 Qy 1798 AATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC 1857  
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 Db 1791 AATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC 1850  
 Qy 1858 ACTTAGGCTTAAAAATGAGCTCA 1880  
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 Db 1851 ACTTAGGCTTAAAAATGAGCTCA 1873

RESULT 14

E15242

LOCUS E15242 1873 bp DNA linear PAT 28-JUL-1999  
 DEFINITION Human mRNA for endothelin B receptor, complete cds.





|    |      |  |      |
|----|------|--|------|
| Qy | 478  | CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC   | 537  |
|    |      |  |      |
| Db | 471  | CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC   | 530  |
| Qy | 538  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC | 597  |
|    |      |  |      |
| Db | 531  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC | 590  |
| Qy | 598  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 657  |
|    |      |  |      |
| Db | 591  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 650  |
| Qy | 658  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 717  |
|    |      |  |      |
| Db | 651  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 710  |
| Qy | 718  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA   | 777  |
|    |      |  |      |
| Db | 711  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA   | 770  |
| Qy | 778  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 837  |
|    |      |  |      |
| Db | 771  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 830  |
| Qy | 838  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA   | 897  |
|    |      |  |      |
| Db | 831  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA   | 890  |
| Qy | 898  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 957  |
|    |      |  |      |
| Db | 891  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 950  |
| Qy | 958  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1017 |
|    |      |  |      |
| Db | 951  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1010 |
| Qy | 1018 | CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTC  | 1077 |
|    |      |  |      |
| Db | 1011 | CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTATTTCAGTTTC  | 1070 |
| Qy | 1078 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATG   | 1137 |
|    |      |  |      |
| Db | 1071 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATG   | 1130 |
| Qy | 1138 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA   | 1197 |
|    |      |  |      |
| Db | 1131 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA   | 1190 |
| Qy | 1198 | GTGGCCAAAACCGTCTTTTGCCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC  | 1257 |
|    |      |  |      |
| Db | 1191 | GTGGCCAAAACCGTCTTTTGCCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC  | 1250 |
| Qy | 1258 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT   | 1317 |
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| Db | 1251 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT   | 1310 |

QY 1318 TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC 1377  
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 Db 1311 TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC 1370  
 QY 1378 ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTGCTTTAAGTCATGC 1437  
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 QY 1438 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC 1497  
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 Db 1491 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC 1550  
 QY 1558 TCATCTTGAAAGAAGAACTATTCAGTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT 1617  
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 Db 1551 TCATCTTGAAAGAAGAACTATTCAGTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT 1610  
 QY 1618 TAAACAAAAATGAAACATTTGCCAAAAACAAAAAACTATGTATTTGCACAGCACAC 1677  
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 Db 1611 TAAACAAAAATGAAACATTTGCCAAAAACAAAAAACTATGTATTTGCACAGCACAC 1670  
 QY 1678 TATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC 1737  
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 Db 1671 TATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC 1730  
 QY 1738 TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1797  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1731 TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1790  
 QY 1798 AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC 1857  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1791 AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC 1850  
 QY 1858 ACTTAGGCTTAAAAATGAGCTCA 1880  
 ||||||||||||||||||||  
 Db 1851 ACTTAGGCTTAAAAATGAGCTCA 1873

RESULT 15

S44866  
 LOCUS S44866 1872 bp mRNA linear PRI 07-MAY-1993  
 DEFINITION ETB endothelin receptor [human, mRNA, 1872 nt].  
 ACCESSION S44866  
 VERSION S44866.1 GI:233233  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1872)  
 AUTHORS Sakamoto,A., Yanagisawa,M., Sakurai,T., Takuwa,Y., Yanagisawa,H.  
 and Masaki,T.  
 TITLE Cloning and functional expression of human cDNA for the ETB  
 endothelin receptor



|    |      |  |      |
|----|------|--|------|
| Qy | 538  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC | 597  |
|    |      |  |      |
| Db | 531  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC | 590  |
| Qy | 598  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 657  |
|    |      |  |      |
| Db | 591  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 650  |
| Qy | 658  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 717  |
|    |      |  |      |
| Db | 651  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 710  |
| Qy | 718  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA   | 777  |
|    |      |  |      |
| Db | 711  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA   | 770  |
| Qy | 778  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 837  |
|    |      |  |      |
| Db | 771  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 830  |
| Qy | 838  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTA    | 897  |
|    |      |  |      |
| Db | 831  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTA    | 890  |
| Qy | 898  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 957  |
|    |      |  |      |
| Db | 891  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 950  |
| Qy | 958  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1017 |
|    |      |  |      |
| Db | 951  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1010 |
| Qy | 1018 | CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTC  | 1077 |
|    |      |  |      |
| Db | 1011 | CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTATTTCAGTTTC  | 1070 |
| Qy | 1078 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG  | 1137 |
|    |      |  |      |
| Db | 1071 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG  | 1130 |
| Qy | 1138 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA   | 1197 |
|    |      |  |      |
| Db | 1131 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA   | 1190 |
| Qy | 1198 | GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC   | 1257 |
|    |      |  |      |
| Db | 1191 | GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC   | 1250 |
| Qy | 1258 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT   | 1317 |
|    |      |  |      |
| Db | 1251 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT   | 1310 |
| Qy | 1318 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC   | 1377 |
|    |      |  |      |
| Db | 1311 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC   | 1370 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1378 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGC    | 1437 |
|    |      |   |      |
| Db | 1371 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGC    | 1430 |
| Qy | 1438 | TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGC   | 1497 |
|    |      |   |      |
| Db | 1431 | TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGC   | 1490 |
| Qy | 1498 | TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGC | 1557 |
|    |      |   |      |
| Db | 1491 | TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGC | 1550 |
| Qy | 1558 | TCATCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT  | 1617 |
|    |      |   |      |
| Db | 1551 | TCATCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT  | 1610 |
| Qy | 1618 | TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC  | 1677 |
|    |      |   |      |
| Db | 1611 | TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC  | 1670 |
| Qy | 1678 | TATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC   | 1737 |
|    |      |   |      |
| Db | 1671 | TATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC   | 1730 |
| Qy | 1738 | TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT  | 1797 |
|    |      |   |      |
| Db | 1731 | TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT  | 1790 |
| Qy | 1798 | AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC  | 1857 |
|    |      |   |      |
| Db | 1791 | AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC  | 1850 |
| Qy | 1858 | ACTTAGGCTTAAAAATGAGCTC  | 1879 |
|    |      |   |      |
| Db | 1851 | ACTTAGGCTTAAAAATGAGCTC  | 1872 |

Search completed: May 14, 2004, 10:14:31  
 Job time : 16263.7 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 23:15:48 ; Search time 1503.76 Seconds  
(without alignments)  
12150.511 Million cell updates/sec

Title: US-09-931-157-2  
Perfect score: 4301  
Sequence: 1 gagacattccggtgggggac.....ctgggaaaaaaaaaaaaaaaa 4301

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB | ID       | Description        |
|------------|--------|-------------|--------|----|----------|--------------------|
| 1          | 4297.8 | 99.9        | 4301   | 2  | AAQ34584 | Aaq34584 ETb recep |
| 2          | 4284.4 | 99.6        | 4286   | 3  | AAA35162 | Aaa35162 Human ade |
| 3          | 4284.4 | 99.6        | 4286   | 3  | AAF21284 | Aaf21284 Human low |
| 4          | 4284.4 | 99.6        | 4286   | 6  | ABV94186 | Abv94186 Breast ca |
| 5          | 4284.4 | 99.6        | 4286   | 7  | ABZ96978 | Abz96978 Human nuc |
| 6          | 4284.4 | 99.6        | 4286   | 7  | ACC72646 | Acc72646 Human end |
| 7          | 4284.4 | 99.6        | 4286   | 7  | ABZ42661 | Abz42661 Human end |

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|---|----|--------|------|--------|---|----------|
|   | 8  | 4284.4 | 99.6 | 4286   | 9 | ADB37423 |
|   | 9  | 4284.4 | 99.6 | 4286   | 9 | ADD18443 |
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|   | 12 | 4284.4 | 99.6 | 13612  | 3 | AAA35166 |
|   | 13 | 4202.4 | 97.7 | 4305   | 8 | ACH03911 |
|   | 14 | 2857   | 66.4 | 2972   | 6 | ABK94410 |
| c | 15 | 2841.8 | 66.1 | 183337 | 7 | ABQ77402 |
|   | 16 | 1691.8 | 39.3 | 1873   | 2 | AAV17875 |
|   | 17 | 1690.8 | 39.3 | 1872   | 3 | AAA35161 |
|   | 18 | 1690.8 | 39.3 | 1872   | 3 | AAF21283 |
|   | 19 | 1690.8 | 39.3 | 1872   | 7 | ABZ96977 |
|   | 20 | 1684.6 | 39.2 | 1892   | 8 | ACH03912 |
|   | 21 | 1676.6 | 39.0 | 1877   | 8 | ACH03913 |
|   | 22 | 1495.4 | 34.8 | 1719   | 3 | AAF21285 |
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|   | 25 | 1466.8 | 34.1 | 1470   | 7 | ACA56605 |
|   | 26 | 1389   | 32.3 | 1632   | 6 | AAD24966 |
|   | 27 | 1322.6 | 30.8 | 1329   | 5 | ABI97988 |
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|   | 31 | 1220.4 | 28.4 | 1578   | 7 | ABZ96981 |
|   | 32 | 1113   | 25.9 | 2018   | 9 | ADB52872 |
|   | 33 | 1099.2 | 25.6 | 1958   | 6 | ABI99321 |
|   | 34 | 1091   | 25.4 | 1965   | 2 | AAQ25892 |
|   | 35 | 1066   | 24.8 | 1406   | 2 | AAQ53922 |
|   | 36 | 763.2  | 17.7 | 800    | 6 | ABS51841 |
|   | 37 | 537.2  | 12.5 | 1752   | 6 | ABK94409 |
| c | 38 | 440.6  | 10.2 | 592    | 6 | ABL63647 |
| c | 39 | 440.6  | 10.2 | 592    | 6 | ABL64653 |
| c | 40 | 440.6  | 10.2 | 592    | 6 | ABN95562 |
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|   | 42 | 395.8  | 9.2  | 1284   | 2 | AAQ63209 |
|   | 43 | 395.8  | 9.2  | 1868   | 3 | AAA34793 |
|   | 44 | 395.8  | 9.2  | 1868   | 3 | AAA34781 |
|   | 45 | 395.8  | 9.2  | 1868   | 3 | AAF20915 |

|          |           |
|----------|-----------|
| Adb37423 | Human can |
| Add18443 | Human pro |
| Aaf21288 | Human low |
| Abz96982 | Human nuc |
| Aaa35166 | Human ade |
| Ach03911 | Human cDN |
| Abk94410 | DNA encod |
| Abq77402 | Human EDN |
| Aav17875 | Homo sapi |
| Aaa35161 | Human ade |
| Aaf21283 | Human low |
| Abz96977 | Human nuc |
| Ach03912 | Human cDN |
| Ach03913 | Human cDN |
| Aaf21285 | Human low |
| Abz96979 | Human nuc |
| Aaa35163 | Human ade |
| Aca56605 | Human sig |
| Aad24966 | Human G-p |
| Abi97988 | Non-endog |
| Abx74409 | Human cDN |
| Aaa35165 | Human ade |
| Aaf21287 | Human low |
| Abz96981 | Human nuc |
| Adb52872 | Primary r |
| Abi99321 | Mouse isc |
| Aaq25892 | Sequence  |
| Aaq53922 | Bovine ET |
| Abs51841 | Novel hum |
| Abk94409 | DNA encod |
| Abl63647 | Breast ca |
| Abl64653 | Stomach c |
| Abn95562 | Gene #206 |
| Ach20099 | Human adu |
| Aaq63209 | Human end |
| Aaa34793 | Human ade |
| Aaa34781 | Human ade |
| Aaf20915 | Human end |

# ALIGNMENTS

## RESULT 1

AAQ34584

ID AAQ34584 standard; DNA; 4301 BP.

XX

AC AAQ34584;

XX

DT 25-MAR-2003 (revised)

DT 11-MAY-1993 (first entry)

XX

DE ETb receptor gene.

XX

KW Human; ETa; ETb; endothelin; receptor; transmembrane domain; N tail;

KW extracellular; cytoplasmic; C tail; post translational; bovine;

KW modification; ET-1 receptor; antagonist; circulatory system; ss.



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XX
OS   Homo sapiens.
XX
FH   Key          Location/Qualifiers
FT   CDS          238. .1566
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FT   sig_peptide  238. .315
FT               /*tag= b
FT   mat_peptide  316. .1563
FT               /*tag= c
FT   misc_feature 1909. .1913
FT               /*tag= i
FT               /function= "Related with mRNA instability"
FT   misc_feature 1997. .2001
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FT   misc_feature 2273. .2277
FT               /*tag= l
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FT   polyA_signal 2595. .2600
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FT   misc_feature 2745. .2749
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FT   polyA_signal 3134. .3139
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FT               /*tag= p
FT               /function= "Related with mRNA instability"
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FT               /*tag= q
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FT   polyA_signal 3638. .3643
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FT   misc_feature 3852. .3856
FT               /*tag= r
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FT   polyA_signal 4101. .4106
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FT   misc_feature 4108. .4112
FT               /*tag= s
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FT   misc_feature 4213. .4217
FT               /*tag= t
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PN      EP522868-A1.
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PD      13-JAN-1993.
XX
PF      10-JUL-1992;    92EP-00306347.
XX
PR      12-JUL-1991;    91JP-00172828.
XX
PA      (SHIO ) SHIONOGI SEIYAKU KK.
XX
PI      Imura H,  Nakao K,  Nakanishi S;
XX
DR      WPI; 1993-010677/02.
DR      P-PSDB; AAR30886.
XX
PT      Human ETa and ETb endothelin receptors - for measuring endothelin and
PT      screening for endothelin antagonists.
XX
PS      Claim 12; Fig 2; 39pp; English.
XX
CC      The sequences given in AAQ34583-84 encode the human ETa and ETb
CC      endothelin receptors respectively. ETa is a 427 amino acid protein with a
CC      molecular weight of 48,726. ETb comprises 442 amino acids and has a
CC      molecular weight of 49,629. ETa has a higher affinity for endothelin (ET)
CC      -1 and ET-2, whereas ETb has no selectivity for ET-1, ET-2 or ET-3. The
CC      receptors each contain seven transmembrane domains and have an
CC      extracellular N tail and a cytoplasmic C tail. There are several
CC      potential sites for post translational modification, these sites are
CC      identical to those of bovine ET-1 receptor. ETa cDNA is 91.2% homologous
CC      to bovine ET-1 receptor cDNA and ETb cDNA is 61.1% homologous to that of
CC      bovine ETa-receptor. The receptor proteins are useful as reagents for
CC      measuring the amount of ET or screening for antagonists of the ET
CC      receptor when studying the circulatory system. (Updated on 25-MAR-2003 to
CC      correct PN field.)
XX
SQ      Sequence 4301 BP; 1342 A; 830 C; 815 G; 1314 T; 0 U; 0 Other;

Query Match          99.9%;  Score 4297.8;  DB 2;  Length 4301;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 4299;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

QY      1  GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

QY      61  AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

QY      121  AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121  AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

QY      181  AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

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|    |      |   |      |
|----|------|---|------|
| Qy | 241  | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGCCTG | 300  |
|    |      |   |      |
| Db | 241  | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGCCTG | 300  |
| Qy | 301  | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360  |
|    |      |   |      |
| Db | 301  | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360  |
| Qy | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420  |
|    |      |   |      |
| Db | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420  |
| Qy | 421  | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480  |
|    |      |   |      |
| Db | 421  | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480  |
| Qy | 481  | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540  |
|    |      |   |      |
| Db | 481  | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540  |
| Qy | 541  | TACATCAACACGGTTGTGTCTGCCTTGTGTTCGTGCTGGGGATCATCGGGAACCTCCACA  | 600  |
|    |      |   |      |
| Db | 541  | TACATCAACACGGTTGTGTCTGCCTTGTGTTCGTGCTGGGGATCATCGGGAACCTCCACA  | 600  |
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660  |
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| Db | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660  |
| Qy | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720  |
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| Db | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720  |
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| Db | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780  |
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|    |      |   |      |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
|    |      |   |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
|    |      |   |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
|    |      |   |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTACAAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTAT | 1080 |
|    |      |   |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTACAAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG | 1140 |

|    |      |  |   |      |
|----|------|--|---|------|
| Db | 1081 |  | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 |  | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Db | 1141 |  | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 |  | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
| Db | 1201 |  | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
| Qy | 1261 |  | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
| Db | 1261 |  | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
| Qy | 1321 |  | AGCTTCTGTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT | 1380 |
| Db | 1321 |  | AGCTTCTGTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT | 1380 |
| Qy | 1381 |  | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
| Db | 1381 |  | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
| Qy | 1441 |  | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
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| Qy | 1501 |  | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
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| Qy | 1561 |  | TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA  | 1620 |
| Db | 1561 |  | TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA  | 1620 |
| Qy | 1621 |  | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
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| Qy | 1681 |  | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Db | 1681 |  | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Qy | 1741 |  | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Db | 1741 |  | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 |  | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
| Db | 1801 |  | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 |  | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
| Db | 1861 |  | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
| Qy | 1921 |  | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
|    |      |  |   |      |

|    |      |   |      |
|----|------|---|------|
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Db | 2161 | TTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTTT   | 2460 |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTTT   | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Db | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Qy | 2641 | GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT    | 2700 |
| Db | 2641 | GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT    | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |

|    |      |   |      |
|----|------|---|------|
| Qy | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAAGTCTTTTGGAGACCGTAAGAACCTCTT | 2880 |
|    |      |   |      |
| Db | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAAGTCTTTTGGAGACCGTAAGAACCTCTT | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
|    |      |   |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
|    |      |   |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
|    |      |   |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
|    |      |   |      |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
| Qy | 3121 | GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA | 3180 |
|    |      |   |      |
| Db | 3121 | GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
|    |      |   |      |
| Db | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAACAATGTGGCCA   | 3300 |
|    |      |   |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAACAATGTGGCCA   | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
|    |      |   |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
| Qy | 3361 | ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |   |      |
| Db | 3361 | ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
|    |      |   |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 3540 |
|    |      |   |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
|    |      |   |      |
| Db | 3541 | TCCTGATACCCTTTCCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
| Qy | 3601 | TGAACTACACACAAAAAGCATACTTGCAATTATTATAATAAAATTGCATTCAGTGGCTT   | 3660 |
|    |      |   |      |
| Db | 3601 | TGAACTACACACAAAAAGCATACTTGCAATTATTATAATAAAATTGCATTCAGTGGCTT   | 3660 |

|    |      |  |      |
|----|------|--|------|
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT  | 3720 |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT  | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT  | 3780 |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT  | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
| Qy | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Db | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
| Qy | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
| Db | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCATAAGTGGCTATAGTTACTGATTT | 4080 |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCATAAGTGGCTATAGTTACTGATTT | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTC | 4140 |
| Db | 4081 | TTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTC | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA | 4200 |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA | 4200 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT | 4260 |
| Db | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT | 4260 |
| Qy | 4261 | AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA                  | 4301 |
| Db | 4261 | AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA                  | 4301 |

# RESULT 2

AAA35162

ID AAA35162 standard; DNA; 4286 BP.

XX

AC AAA35162;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:36.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;

KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200009525-A2.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 03-AUG-1999; 99WO-US017712.  
 XX  
 PR 03-AUG-1998; 98US-0095212P.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 PI Nyce JW;  
 XX  
 DR WPI; 2000-205971/18.  
 XX  
 PT New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers.  
 XX  
 PS Disclosure; Page 1191-1192; 1343pp; English.  
 XX  
 CC The present invention describes a new composition comprising an antisense  
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 CC nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 CC impeded respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 CC carcinomas, and cancers which may metastasise to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of the  
 CC ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
 CC Sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 CC listing  
 XX  
 SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;



Query Match 99.6%; Score 4284.4; DB 3; Length 4286;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60
      |||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
      |||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
      |||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240
      |||
Db    181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300
      |||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
      |||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
      |||
Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
      |||
Db    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540
      |||
Db    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540

Qy    541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCCACA 600
      |||
Db    541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCCACA 600

Qy    601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660
      |||
Db    601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660

Qy    661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720
      |||
Db    661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720

Qy    721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780
      |||
Db    721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780
```

Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840

Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTCCAAAATGGACAGCAGTAGAA 900  
 |||||  
 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTCCAAAATGGACAGCAGTAGAA 900

Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 |||||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960

Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020  
 |||||  
 Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020

Qy 1021 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCACTTTCTAT 1080  
 |||||  
 Db 1021 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCACTTTCTAT 1080

Qy 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 |||||  
 Db 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG 1140

Qy 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 |||||  
 Db 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200

Qy 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCTTCACCTC 1260  
 |||||  
 Db 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCTTCACCTC 1260

Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTG 1320  
 |||||  
 Db 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTG 1320

Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 |||||  
 Db 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380

Qy 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA 1440  
 |||||  
 Db 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA 1440

Qy 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGCTTA 1500  
 |||||  
 Db 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGCTTA 1500

Qy 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA 1560  
 |||||  
 Db 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA 1560

Qy 1561 TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA 1620  
 |||||  
 Db 1561 TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA 1620

Qy 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAGCTATGTATTTGCACAGCACACTAT 1680

|    |      |   |      |
|----|------|---|------|
| Db | 1621 | <br>AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT      | 1740 |
| Db | 1681 | <br>TAAAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT      | 1800 |
| Db | 1741 | <br>TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT      | 1860 |
| Db | 1801 | <br>TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA     | 1920 |
| Db | 1861 | <br>TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG       | 1980 |
| Db | 1921 | <br>AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAACAACTTTTCAATTAATAT       | 2040 |
| Db | 1981 | <br>AAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAACAACTTTTCAATTAATAT   | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT      | 2100 |
| Db | 2041 | <br>TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT      | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTCTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC        | 2220 |
| Db | 2161 | <br>TTTTGAAAATCATTACACTTTTCTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC    | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA      | 2280 |
| Db | 2221 | <br>CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTAAAGATCAAACCTCA       | 2340 |
| Db | 2281 | <br>TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTAAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA       | 2400 |
| Db | 2341 | <br>CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTT      | 2460 |
| Db | 2401 | <br>CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTT  | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA      | 2520 |
|    |      |   |      |

Db 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 Qy 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Db 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Qy 2581 GCCAGTGACCTCATAATAAAGACTGTGAACCTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Db 2581 GCCAGTGACCTCATAATAAAGACTGTGAACCTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Qy 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 Db 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 Qy 2701 GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760  
 Db 2701 GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760  
 Qy 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 Qy 2821 ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Db 2821 ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 Qy 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 Db 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 Qy 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 Db 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 Qy 3181 ATTTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 Db 3181 ATTTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 Qy 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAATGTGGCCA 3300  
 Db 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAATGTGGCCA 3300  
 Qy 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360

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|----|------|---|------|
| Qy | 3361 | ACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Db | 3361 | ACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTAAGTGAATTTTACA   | 3540 |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTAAGTGAATTTTACA   | 3540 |
| Qy | 3541 | TCCTGATACCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT    | 3600 |
| Db | 3541 | TCCTGATACCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT    | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTGAGTGGCTT  | 3660 |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTGAGTGGCTT  | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Db | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
| Db | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC    | 4140 |
| Db | 4081 | TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC    | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTTAAAGAAATATAAATGTGA  | 4200 |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTTAAAGAAATATAAATGTGA  | 4200 |

QY 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 QY 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 ||||||||||||||||||||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 3

AAF21284

ID AAF21284 standard; DNA; 4286 BP.

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AC AAF21284;

XX

DT 14-MAR-2001 (first entry)

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DE Human low adenosine antisense oligonucleotide related sequence #2851.

XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200062736-A2.

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PD 26-OCT-2000.

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PF 24-MAR-2000; 2000WO-US008020.

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PR 06-APR-1999; 99US-0127958P.

XX

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

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PI Nyce JW;

XX

DR WPI; 2000-679539/66.

XX

PT Low adenosine (A) content antisense oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.

XX

PS Disclosure; Page 1273-1274; 1592pp; English.

XX

CC The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,

CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention

XX

SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;

Query Match 99.6%; Score 4284.4; DB 3; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
|    |     |   |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
| QY | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
|    |     |   |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| QY | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
|    |     |   |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
| QY | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
|    |     |   |     |
| Db | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
| QY | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300 |
|    |     |   |     |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300 |
| QY | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCTGACAGGGCCACTCCGCTTTTGCAA   | 360 |
|    |     |   |     |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCTGACAGGGCCACTCCGCTTTTGCAA   | 360 |
| QY | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |

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|    |  |      |
| Db | 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTCCAACGCCAGT    | 420  |
| Qy | 421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG   | 480  |
| Db | 421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG   | 480  |
| Qy | 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA    | 540  |
| Db | 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA    | 540  |
| Qy | 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA   | 600  |
| Db | 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA   | 600  |
| Qy | 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Db | 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Qy | 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Db | 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Qy | 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Db | 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Qy | 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Db | 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Qy | 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Db | 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Qy | 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
| Db | 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
| Qy | 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG  | 1020 |
| Db | 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG  | 1020 |
| Qy | 1021 AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Db | 1021 AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG | 1140 |
| Db | 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG | 1140 |
| Qy | 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Db | 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 GCCAAAACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
|    |  |      |



Db 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260  
 Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG 1320  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG 1320  
 Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 Qy 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA 1440  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA 1440  
 Qy 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500  
 Qy 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA 1560  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA 1560  
 Qy 1561 TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTTCTTTATATTGGACCGAAGTCATTAA 1620  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1561 TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTTCTTTATATTGGACCGAAGTCATTAA 1620  
 Qy 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT 1680  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT 1680  
 Qy 1681 TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT 1740  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1681 TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT 1740  
 Qy 1741 TTACGGCATGGAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT 1800  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1741 TTACGGCATGGAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT 1800  
 Qy 1801 TTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT 1860  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1801 TTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT 1860  
 Qy 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT 1920  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT 1920  
 Qy 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACCTTTTAAATG 1980  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACCTTTTAAATG 1980  
 Qy 1981 AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACCTTTTCAATTAATAT 2040  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1981 AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACCTTTTCAATTAATAT 2040  
 Qy 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT 2100  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT 2100

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|----|------|--|------|
| QY | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
|    |      |  |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
| QY | 2161 | TTTTGAAAATCATTACACTTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
|    |      |  |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| QY | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA   | 2280 |
|    |      |  |      |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA   | 2280 |
| QY | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA  | 2340 |
|    |      |  |      |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA  | 2340 |
| QY | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA    | 2400 |
|    |      |  |      |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA    | 2400 |
| QY | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT   | 2460 |
|    |      |  |      |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT   | 2460 |
| QY | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCTATCTGTAAATACTTACCTACATACA  | 2520 |
|    |      |  |      |
| Db | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCTATCTGTAAATACTTACCTACATACA  | 2520 |
| QY | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
|    |      |  |      |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
| QY | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
|    |      |  |      |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
| QY | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT   | 2700 |
|    |      |  |      |
| Db | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT   | 2700 |
| QY | 2701 | GCTATAGTTAAAATACTATTTTTTCAAAATCATAACAGATTAGTACATTTAACAGCTACCTG | 2760 |
|    |      |  |      |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTTCAAAATCATAACAGATTAGTACATTTAACAGCTACCTG | 2760 |
| QY | 2761 | TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
|    |      |  |      |
| Db | 2761 | TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
| QY | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTTGAGACCGTAAGAACCTCTT  | 2880 |
|    |      |  |      |
| Db | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTTGAGACCGTAAGAACCTCTT  | 2880 |
| QY | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
|    |      |  |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |

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|----|------|---|------|
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA   | 3180 |
| Db | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA   | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG  | 3240 |
| Db | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG  | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA   | 3300 |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA   | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
| Qy | 3361 | ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Db | 3361 | ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 3540 |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
| Db | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
| Qy | 3781 | TTCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |

|    |      |  |  |      |
|----|------|--|--|------|
| Db | 3781 |  | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
| Qy | 3841 |  | CAGCTCAAAGATTATATAAGATTTTAACCTATTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
| Db | 3841 |  | CAGCTCAAAGATTATATAAGATTTTAACCTATTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
| Qy | 3901 |  | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
| Db | 3901 |  | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
| Qy | 3961 |  | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT | 4020 |
| Db | 3961 |  | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT | 4020 |
| Qy | 4021 |  | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT | 4080 |
| Db | 4021 |  | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT | 4080 |
| Qy | 4081 |  | TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC    | 4140 |
| Db | 4081 |  | TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC    | 4140 |
| Qy | 4141 |  | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA  | 4200 |
| Db | 4141 |  | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA  | 4200 |
| Qy | 4201 |  | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT | 4260 |
| Db | 4201 |  | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT | 4260 |
| Qy | 4261 |  | AAAATGCCACATTTCTGGTCTCTGGG                                   | 4286 |
| Db | 4261 |  | AAAATGCCACATTTCTGGTCTCTGGG                                   | 4286 |

# RESULT 4

ABV94186

ID ABV94186 standard; cDNA; 4286 BP.

XX

AC ABV94186;

XX

DT 08-JAN-2003 (first entry)

XX

DE Breast carcinoma related nucleotide sequence SEQ ID NO:177.

XX

KW Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;  
KW ss.

XX

OS Homo sapiens.

XX

PN WO200246467-A2.

XX

PD 13-JUN-2002.

XX

PF 07-DEC-2001; 2001WO-IB002811.

XX

PR 08-DEC-2000; 2000US-0254090P.  
PR 07-DEC-2001; 2001US-00007926.

XX  
PA (IPSO-) IPSOGEN.

XX Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;  
PI  
XX  
DR WPI; 2002-619023/66.

XX  
PT Novel polynucleotide library useful in molecular characterization of a  
PT carcinoma, comprising a pool of polynucleotide sequences or its  
PT subsequences which are either underexpressed or overexpressed in tumor  
PT cells.

XX  
PS Claim 1; Page 225-226; 401pp; English.

XX The present invention describes a polynucleotide library (I) useful in  
CC the molecular characterisation of a carcinoma, comprising a pool of  
CC polynucleotides or its subsequences which are either underexpressed or  
CC overexpressed in tumour cells, and correspond to any of the  
CC polynucleotide sequences chosen from the 468 sequences given in ABV94010  
CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for  
CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting  
CC (M1) differentially expressed polynucleotide sequences which are  
CC correlated with a cancer, involves obtaining a polynucleotide sample from  
CC a patient, and reacting the polynucleotide sample obtained with a probe  
CC immobilised on a solid support, where the probe comprises any combination  
CC of the polynucleotide sequences of (I) or its expression products encoded  
CC by polynucleotide sequences of (I), and detecting the reaction product.  
CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)  
CC is useful in molecular characterisation of a carcinoma. (I) and (II) are  
CC useful for the prognosis or diagnostic of tumour, in differentiating a  
CC normal cell from a cancer cell, detecting a hormone sensitive tumour  
CC cell, differentiating a tumour with lymph nodes from a tumour without  
CC lymph nodes, differentiating antracycline-sensitive tumours from  
CC antracycline-insensitive tumours, and classifying good and poor prognosis  
CC primary breast tumours. (I) is useful for large-scale molecular  
CC characterisation of breast cancer that help in prediction, prognosis and  
CC cancer treatment, and for detecting differentially expressed genes that  
CC correlated with a cancer

XX  
SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;

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Query Match          99.6%; Score 4284.4; DB 6; Length 4286;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
|    |     |  |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
|    |     |  |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGAGTCTGGACATCTGA  | 180 |
|    |     |  |     |

Db 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180  
 Qy 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
 Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300  
 Qy 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360  
 Qy 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420  
 Qy 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
 Qy 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTTCAA 540  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTTCAA 540  
 Qy 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAGTCCACA 600  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAGTCCACA 600  
 Qy 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020

|    |      |  |      |
|----|------|--|------|
| Qy | 1021 | AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
|    |      |  |      |
| Db | 1021 | AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
|    |      |  |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
|    |      |  |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC     | 1260 |
|    |      |  |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC     | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTG   | 1320 |
|    |      |  |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
|    |      |  |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
|    |      |  |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
|    |      |  |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCCTGTATTTTCTTTATATTGGACCGAAGTCATTAA         | 1620 |
|    |      |  |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCCTGTATTTTCTTTATATTGGACCGAAGTCATTAA         | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAGTATGTATTTGCACAGCACACTAT     | 1680 |
|    |      |  |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAGTATGTATTTGCACAGCACACTAT     | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
|    |      |  |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
|    |      |  |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT   | 1860 |
|    |      |  |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT   | 1860 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA | 1920 |
| Db | 1861 |   |      |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA | 1920 |
| Db |      |   |      |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
| Db | 1921 |   |      |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
| Db |      |   |      |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACTTTTCAATTAATAT  | 2040 |
| Db | 1981 |   |      |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACTTTTCAATTAATAT  | 2040 |
| Db |      |   |      |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Db | 2041 |   |      |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Db |      |   |      |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Db | 2101 |   |      |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Db |      |   |      |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC   | 2220 |
| Db | 2161 |   |      |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC   | 2220 |
| Db |      |   |      |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Db | 2221 |   |      |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Db |      |   |      |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Db | 2281 |   |      |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Db |      |   |      |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Db | 2341 |   |      |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Db |      |   |      |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 2460 |
| Db | 2401 |   |      |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 2460 |
| Db |      |   |      |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Db | 2461 |   |      |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Db |      |   |      |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Db | 2521 |   |      |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Db |      |   |      |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Db | 2581 |   |      |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Db |      |   |      |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 2700 |
| Db | 2641 |   |      |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 2700 |
| Db |      |   |      |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |



|    |      |  |      |
|----|------|--|------|
| Db | 2701 | <br>GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG    | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG       | 2820 |
| Db | 2761 | <br>TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT       | 2880 |
| Db | 2821 | <br>ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT   | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT       | 2940 |
| Db | 2881 | <br>AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG       | 3000 |
| Db | 2941 | <br>GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT      | 3060 |
| Db | 3001 | <br>GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA        | 3120 |
| Db | 3061 | <br>CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA        | 3180 |
| Db | 3121 | <br>GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA    | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTTCTTTTAAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG      | 3240 |
| Db | 3181 | <br>ATTTTTACTTTGTTTTTCTTTTAAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG  | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCA       | 3300 |
| Db | 3241 | <br>TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCA   | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC       | 3360 |
| Db | 3301 | <br>GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT     | 3420 |
| Db | 3361 | <br>ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA       | 3480 |
| Db | 3421 | <br>CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA        | 3540 |
| Db | 3481 | <br>TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA    | 3540 |
| Qy | 3541 | TCCTGATACCCTTTTCCTTCTCCATGTCAAGTATCATGTTCTCTAATTATCTTGCCAAATTT     | 3600 |
|    |      |  |      |

|    |      |   |      |
|----|------|---|------|
| Db | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Db | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
| Db | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAACTACCTTATTTTTT      | 4140 |
| Db | 4081 | TTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAACTACCTTATTTTTT      | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA  | 4200 |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA  | 4200 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT  | 4260 |
| Db | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT  | 4260 |
| Qy | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                    | 4286 |
| Db | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                    | 4286 |

RESULT 5

ABZ96978

ID ABZ96978 standard; DNA; 4286 BP.

XX

AC ABZ96978;

XX

DT 17-OCT-2003 (first entry)  
 XX  
 DE Human nucleic acid sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 12220; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;

Query Match 99.6%; Score 4284.4; DB 7; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
|    |     |   |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
|    |     |   |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
|    |     |   |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
|    |     |   |     |
| Db | 181 | AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG   | 300 |
|    |     |   |     |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG   | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
|    |     |   |     |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
|    |     |   |     |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
| Qy | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
|    |     |   |     |
| Db | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540 |
|    |     |   |     |
| Db | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540 |
| Qy | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA | 600 |
|    |     |   |     |
| Db | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA | 600 |
| Qy | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
|    |     |   |     |
| Db | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
| Qy | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
|    |     |   |     |
| Db | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
| Qy | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |
|    |     |   |     |
| Db | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |

Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840

Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 |||  
 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900

Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 |||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960

Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020  
 |||  
 Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020

Qy 1021 AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080  
 |||  
 Db 1021 AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080

Qy 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 |||  
 Db 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG 1140

Qy 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 |||  
 Db 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200

Qy 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260  
 |||  
 Db 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260

Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG 1320  
 |||  
 Db 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG 1320

Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 |||  
 Db 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380

Qy 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA 1440  
 |||  
 Db 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA 1440

Qy 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500  
 |||  
 Db 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500

Qy 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA 1560  
 |||  
 Db 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA 1560

Qy 1561 TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA 1620  
 |||  
 Db 1561 TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA 1620

Qy 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAAGTATGTATTTGCACAGCACACTAT 1680

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|----|------|--|------|
| Db | 1621 | <br>AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT | 1680 |
| Qy | 1681 | TAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT       | 1740 |
| Db | 1681 | <br>TAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT     | 1800 |
| Db | 1741 | <br>TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT     | 1860 |
| Db | 1801 | <br>TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT       | 1920 |
| Db | 1861 | <br>TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT   | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG      | 1980 |
| Db | 1921 | <br>AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG  | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTTTCAATTAATAT        | 2040 |
| Db | 1981 | <br>AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTTTCAATTAATAT    | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT     | 2100 |
| Db | 2041 | <br>TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT     | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC     | 2220 |
| Db | 2161 | <br>TTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA     | 2280 |
| Db | 2221 | <br>CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA      | 2340 |
| Db | 2281 | <br>TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA  | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA      | 2400 |
| Db | 2341 | <br>CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA  | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTT     | 2460 |
| Db | 2401 | <br>CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTT | 2460 |
| Qy | 2461 | TCATATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA      | 2520 |
|    |      |  |      |

Db 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 Qy 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Qy 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Qy 2641 GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2641 GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 Qy 2701 GCTATAGTTAAAATACTATTTTTTCAAAATCATAACAGATTAGTACATTTAACAGCTACCTG 2760  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2701 GCTATAGTTAAAATACTATTTTTTCAAAATCATAACAGATTAGTACATTTAACAGCTACCTG 2760  
 Qy 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 Qy 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 Qy 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 Qy 3121 GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3121 GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 Qy 3181 ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3181 ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 Qy 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
 Qy 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360

Qy 3361 ACAAACCTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 |||  
 Db 3361 ACAAACCTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420

Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 |||  
 Db 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480

Qy 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTAATTTTACA 3540  
 |||  
 Db 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTAATTTTACA 3540

Qy 3541 TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 |||  
 Db 3541 TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600

Qy 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660  
 |||  
 Db 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660

Qy 3661 TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 |||  
 Db 3661 TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720

Qy 3721 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780  
 |||  
 Db 3721 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 |||  
 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840

Qy 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 |||  
 Db 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 |||  
 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 |||  
 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 |||  
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080

Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTC 4140  
 |||  
 Db 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTC 4140

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 |||  
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200



QY 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 ||||||||||||||||||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 QY 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 ||||||||||||||||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 6

ACC72646

ID ACC72646 standard; cDNA; 4286 BP.

XX

AC ACC72646;

XX

DT 09-JUL-2003 (first entry)

XX

DE Human endothelin receptor type B encoding cDNA.

XX

KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;  
 KW heart disease; atherosclerosis; endometriosis; gene; ss.

XX

OS Homo sapiens.

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PN WO2003025138-A2.

XX

PD 27-MAR-2003.

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PF 17-SEP-2002; 2002WO-US029560.

XX

PR 17-SEP-2001; 2001US-0323469P.

PR 20-SEP-2001; 2001US-0323887P.

PR 13-NOV-2001; 2001US-0350666P.

PR 08-FEB-2002; 2002US-0355145P.

PR 08-FEB-2002; 2002US-0355257P.

PR 12-APR-2002; 2002US-0372246P.

XX

PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX

PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;

PI Zlotnik A;

XX

DR WPI; 2003-354600/33.

DR P-PSDB; ABR58526.

XX

PT New genes that are up-regulated or down-regulated in cancers, useful as  
 PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as  
 PT therapeutic targets for screening drugs for treating these diseases.

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PS Claim 8; Page 143-144; 767pp; English.

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CC The present invention describes an isolated nucleic acid molecule, which  
 CC comprises the sequence of any of the genes that are up-regulated or down-  
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in  
 CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer  
 CC related gene nucleotide sequences which encode the proteins given in  
 CC ABR58521 to ABR58709. Also described: (1) determining the presence or

CC absence of a pathological cell in a patient; (2) an expression vector  
 CC comprising a nucleic acid molecule described above; (3) a host cell  
 CC comprising the vector; (4) an isolated polypeptide, which is encoded by  
 CC the nucleic acid; (5) an antibody that specifically binds the polypeptide  
 CC of (4); (6) specifically targeting a compound to a pathological cell in a  
 CC patient by administering to the patient the antibody above; and (7) a  
 CC drug screening assay. The nucleic acid is useful as diagnostic markers or  
 CC therapeutic targets. In particular, the nucleic acid is useful for  
 CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,  
 CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,  
 CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,  
 CC atherosclerosis and endometriosis. The nucleic acid is also useful in  
 CC drug screening, particularly for identifying agents for treating these  
 CC pathologies

XX

SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;

Query Match 99.6%; Score 4284.4; DB 7; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
|    |     |  |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
|    |     |  |     |
| Db | 61  | AGGTAGGCATTTGCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA | 180 |
|    |     |  |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG | 240 |
|    |     |  |     |
| Db | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG | 240 |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG | 300 |
|    |     |  |     |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA | 360 |
|    |     |  |     |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT | 420 |
|    |     |  |     |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT | 420 |
| Qy | 421 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
|    |     |  |     |
| Db | 421 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |
|    |     |  |     |
| Db | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |

Qy 541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGCTGGGGATCATCGGGAACCTCCACA 600  
 |||  
 Db 541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGCTGGGGATCATCGGGAACCTCCACA 600  
 |||  
 Qy 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 |||  
 Db 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 |||  
 Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 |||  
 Db 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 |||  
 Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 |||  
 Db 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 |||  
 Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||  
 Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 |||  
 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 |||  
 Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 |||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 |||  
 Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG 1020  
 |||  
 Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG 1020  
 |||  
 Qy 1021 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080  
 |||  
 Db 1021 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080  
 |||  
 Qy 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 |||  
 Db 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 |||  
 Qy 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 |||  
 Db 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 |||  
 Qy 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTC 1260  
 |||  
 Db 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTC 1260  
 |||  
 Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG 1320  
 |||  
 Db 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG 1320  
 |||  
 Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 |||  
 Db 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 |||  
 Qy 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA 1440

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|----|---|------|
|    |   |      |
| Db | 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA     | 1440 |
| Qy | 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
| Db | 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
| Qy | 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Db | 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Qy | 1561 TCTTGAAAGAAGAACTATTTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
| Db | 1561 TCTTGAAAGAAGAACTATTTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
| Qy | 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAAGCTATGTATTTGCACAGCACACTAT  | 1680 |
| Db | 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAAGCTATGTATTTGCACAGCACACTAT  | 1680 |
| Qy | 1681 TAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Db | 1681 TAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Qy | 1741 TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Db | 1741 TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 TTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT    | 1860 |
| Db | 1801 TTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT    | 1860 |
| Qy | 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT     | 1920 |
| Db | 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT     | 1920 |
| Qy | 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG   | 1980 |
| Db | 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 AAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT   | 2040 |
| Db | 1981 AAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT   | 2040 |
| Qy | 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
| Db | 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
| Qy | 2101 TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
| Db | 2101 TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
| Qy | 2161 TTTTGAAATCATTACACTTTCACTAGAAGCCCCAACCTCAGCATTCTGCAATATGTAAC    | 2220 |
| Db | 2161 TTTTGAAATCATTACACTTTCACTAGAAGCCCCAACCTCAGCATTCTGCAATATGTAAC    | 2220 |
| Qy | 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA   | 2280 |
|    |   |      |

Db 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA 2280  
 Qy 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA 2340  
 Db 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA 2340  
 Qy 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA 2400  
 Db 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA 2400  
 Qy 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT 2460  
 Db 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT 2460  
 Qy 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 Db 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 Qy 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Db 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Qy 2581 GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Db 2581 GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Qy 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 Db 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 Qy 2701 GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760  
 Db 2701 GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760  
 Qy 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 Qy 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Db 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCTTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCTTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 Qy 3061 CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAACACAGTGCAATGTTCTCA 3120  
 Db 3061 CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAACACAGTGCAATGTTCTCA 3120

Qy 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180

Qy 3181 ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3181 ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240

Qy 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300

Qy 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360

Qy 3361 ACAAACTTGTTCCTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3361 ACAAACTTGTTCCTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420

Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480

Qy 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTTACA 3540  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTTACA 3540

Qy 3541 TCCTGATACCCTTTCTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3541 TCCTGATACCCTTTCTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600

Qy 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT 3660  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT 3660

Qy 3661 TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3661 TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720

Qy 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840

Qy 3841 CAGCTCAAAGATTATATAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3841 CAGCTCAAAGATTATATAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAAGTGTAATATAACAATGT 4020  
 |||  
 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAAGTGTAATATAACAATGT 4020  
 Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 |||  
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTC 4140  
 |||  
 Db 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTC 4140  
 Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 |||  
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 |||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 |||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

# RESULT 7

ABZ42661

ID ABZ42661 standard; DNA; 4286 BP.

XX

AC ABZ42661;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human endothelin B receptor nucleotide SEQ ID NO:113.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US050107.

XX

PR 19-DEC-2000; 2000US-0257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
 XX  
 PI Burmer GC, Roush CL, Brown JP;  
 XX  
 DR WPI; 2003-046718/04.  
 DR P-PSDB; ABP81815.  
 XX  
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Fig 1; 523pp; English.  
 XX  
 CC The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;

Query Match 99.6%; Score 4284.4; DB 7; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
|    |     |  |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
| QY | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
|    |     |  |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
| QY | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA | 180 |
|    |     |  |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA | 180 |



|    |     |  |      |
|----|-----|--|------|
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240  |
|    |     |  |      |
| Db | 181 | AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240  |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG   | 300  |
|    |     |  |      |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG   | 300  |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA   | 360  |
|    |     |  |      |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA   | 360  |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 420  |
|    |     |  |      |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 420  |
| Qy | 421 | CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG  | 480  |
|    |     |  |      |
| Db | 421 | CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG  | 480  |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA     | 540  |
|    |     |  |      |
| Db | 481 | CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA     | 540  |
| Qy | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA | 600  |
|    |     |  |      |
| Db | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA | 600  |
| Qy | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
|    |     |  |      |
| Db | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Qy | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
|    |     |  |      |
| Db | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Qy | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
|    |     |  |      |
| Db | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Qy | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
|    |     |  |      |
| Db | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Qy | 841 | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
|    |     |  |      |
| Db | 841 | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Qy | 901 | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
|    |     |  |      |
| Db | 901 | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
| Qy | 961 | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
|    |     |  |      |
| Db | 961 | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |

|    |      |  |      |
|----|------|--|------|
| Qy | 1021 | AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
|    |      |  |      |
| Db | 1021 | AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
|    |      |  |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Qy | 1141 | AGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
|    |      |  |      |
| Db | 1141 | AGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCCTGGTCCTTGCTTTGCCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
|    |      |  |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCCTGGTCCTTGCTTTGCCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
|    |      |  |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
|    |      |  |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
|    |      |  |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
|    |      |  |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA  | 1620 |
|    |      |  |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA  | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT    | 1680 |
|    |      |  |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT    | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
|    |      |  |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
|    |      |  |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT   | 1860 |
|    |      |  |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT   | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT     | 1920 |

|    |      |   |      |
|----|------|---|------|
| Db | 1861 | <br>TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG       | 1980 |
| Db | 1921 | <br>AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT      | 2040 |
| Db | 1981 | <br>AAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT  | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT      | 2100 |
| Db | 2041 | <br>TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT      | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC     | 2220 |
| Db | 2161 | <br>TTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA      | 2280 |
| Db | 2221 | <br>CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA       | 2340 |
| Db | 2281 | <br>TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA       | 2400 |
| Db | 2341 | <br>CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATAATCTTCTTTT      | 2460 |
| Db | 2401 | <br>CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATAATCTTCTTTT  | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTGTGCATCTGTAAATACTTACCTACATACA      | 2520 |
| Db | 2461 | <br>TCACTATCGTAGCTTAAACTCTGTTTGGTTTGTGCATCTGTAAATACTTACCTACATACA  | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT      | 2580 |
| Db | 2521 | <br>CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG      | 2640 |
| Db | 2581 | <br>GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Qy | 2641 | GCAGGTAGCACCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT         | 2700 |
| Db | 2641 | <br>GCAGGTAGCACCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT     | 2700 |
| Qy | 2701 | GCTATAGTTAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG       | 2760 |
|    |      |   |      |

Db 2701 GCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760  
 Qy 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 Qy 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCCAAAAGTCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Db 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCCAAAAGTCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 Qy 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 Db 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 Qy 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 Db 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 Qy 3181 ATTTTTACTTTGTTTTCTTTTAAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 Db 3181 ATTTTTACTTTGTTTTCTTTTAAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 Qy 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
 Db 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
 Qy 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 Qy 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 Db 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 Db 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 Qy 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA 3540  
 Db 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA 3540  
 Qy 3541 TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 Db 3541 TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600

|    |      |   |      |
|----|------|---|------|
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
|    |      |   |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
| Qy | 3661 | TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
|    |      |   |      |
| Db | 3661 | TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
|    |      |   |      |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
|    |      |   |      |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
| Qy | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT   | 3900 |
|    |      |   |      |
| Db | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT   | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
|    |      |   |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
| Qy | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT   | 4020 |
|    |      |   |      |
| Db | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT   | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
|    |      |   |      |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTC | 4140 |
|    |      |   |      |
| Db | 4081 | TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTC | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA  | 4200 |
|    |      |   |      |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA  | 4200 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT  | 4260 |
|    |      |   |      |
| Db | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT  | 4260 |
| Qy | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                    | 4286 |
|    |      |   |      |
| Db | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                    | 4286 |

RESULT 8

ADB37423

ID ADB37423 standard; DNA; 4286 BP.

XX

AC ADB37423;

XX

DT 04-DEC-2003 (first entry)

XX  
 DE Human cancer associated gene EDNRB polynucleotide #2.  
 XX  
 KW antisense therapy; gene therapy; cytostatic; cancer; Wnt5a; MART-1;  
 KW pirin; HADHB; CD63; ENDRB; PGAM1; HXB; RXRA; integrin b1; syndecan 4;  
 KW tropomyosin 1; AXL; EphA2; GAP43; PFKL; synuclein a; annexin A2; CD20;  
 KW RAB2; tumour; malignant melanoma;  
 KW wingless MMTV integration site family member 5a; human; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003152923-A1.  
 XX  
 PD 14-AUG-2003.  
 XX  
 PF 02-AUG-2001; 2001US-00921406.  
 XX  
 PR 02-AUG-2001; 2001US-00921406.  
 XX  
 PA (YAKH/) YAKHINI Z.  
 PA (BITT/) BITTNER M.  
 PA (TREN/) TRENT J.  
 PA (BEND/) BEN-DOR A.  
 PA (MELT/) MELTZER P.  
 PA (CHEN/) CHEN Y.  
 PA (WEER/) WEERARATNA A.  
 PA (JIAN/) JIANG Y.  
 PA (SAMP/) SAMPAS N.  
 PA (DOUG/) DOUGHERTY E.  
 XX  
 PI Yakhini Z, Bittner M, Trent J, Ben-Dor A, Meltzer P, Chen Y;  
 PI Weeraratna A, Jiang Y, Sampas N, Dougherty E;  
 XX  
 DR WPI; 2003-635998/60.  
 XX  
 PT Diagnosing an aggressive form of cancer, comprises detecting expression  
 PT pattern of genes such as Wnt5a, MART-1, pirin, HADHB, CD63, ENDRB, PGAM1,  
 PT synuclein a, annexin A2, CD20, and RAB2.  
 XX  
 PS Disclosure; Page 27-29; 70pp; English.  
 XX  
 CC The invention describes a method of diagnosing an aggressive form of  
 CC cancer comprising: analysing expression of genes Wnt5a, MART-1, pirin,  
 CC HADHB, CD63, ENDRB, PGAM1, HXB, RXRA, integrin b1, syndecan 4,  
 CC tropomyosin 1, AXL, EphA2, GAP43, PFKL, synuclein a, annexin A2, CD20,  
 CC and RAB2 in tumour sample; and identifying the tumour as aggressive or  
 CC non-aggressive based on the expression pattern of the genes. The methods  
 CC are useful for detecting and treating malignant melanoma found to be  
 CC associated with gene markers such as Wnt5a. This sequence represents a  
 CC polynucleotide of a human gene, the expression level of which is used in  
 CC cancer diagnosis.  
 XX  
 SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;  
  
 Query Match 99.6%; Score 4284.4; DB 9; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCCGTGG | 120 |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCCGTGG | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGAGTCTGGACATCTGA   | 180 |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGAGTCTGGACATCTGA   | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240 |
| Db | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240 |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGTTGCGCTGGTTCTTGCCTGCGGCCTG   | 300 |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGTTGCGCTGGTTCTTGCCTGCGGCCTG   | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
| Qy | 421 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG  | 480 |
| Db | 421 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG  | 480 |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540 |
| Db | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540 |
| Qy | 541 | TACATCAACACGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCCACA  | 600 |
| Db | 541 | TACATCAACACGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCCACA  | 600 |
| Qy | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
| Db | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
| Qy | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
| Db | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
| Qy | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |
| Db | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |
| Qy | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840 |
| Db | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840 |

|    |      |  |      |
|----|------|--|------|
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCAAAAATGGACAGCAGTAGAA   | 900  |
|    |      |  |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCAAAAATGGACAGCAGTAGAA   | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
|    |      |  |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
|    |      |  |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTAT | 1080 |
|    |      |  |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
|    |      |  |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
|    |      |  |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTC    | 1260 |
|    |      |  |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTC    | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
|    |      |  |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
|    |      |  |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
|    |      |  |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
|    |      |  |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTTATATTGGACCGAAGTCATTAA       | 1620 |
|    |      |  |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTTATATTGGACCGAAGTCATTAA       | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT    | 1680 |
|    |      |  |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT    | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT      | 1740 |



|    |      |   |      |
|----|------|---|------|
| Db | 1681 | <br>TAAAAATATTAAGTGTAAATTATTTTAACTACTCACAGCTACATATGACATTTTATGAGCTGT | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT        | 1800 |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT        | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT        | 1860 |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT        | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT          | 1920 |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT          | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTAAATG         | 1980 |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTAAATG         | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT          | 2040 |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT          | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT        | 2100 |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT        | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT        | 2160 |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT        | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC        | 2220 |
| Db | 2161 | TTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC        | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA        | 2280 |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA        | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA         | 2340 |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA         | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA         | 2400 |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA         | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATACTTCTTTTT         | 2460 |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATACTTCTTTTT         | 2460 |
| Qy | 2461 | TCATATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA         | 2520 |
| Db | 2461 | TCATATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA         | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT        | 2580 |

|    |      |  |      |
|----|------|--|------|
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
|    |      |  |      |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 2700 |
|    |      |  |      |
| Db | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
|    |      |  |      |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
|    |      |  |      |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGGAGACCGTAAGAACCTCTT    | 2880 |
|    |      |  |      |
| Db | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGGAGACCGTAAGAACCTCTT    | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
|    |      |  |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
|    |      |  |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
|    |      |  |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
|    |      |  |      |
| Db | 3061 | CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
| Qy | 3121 | GAGTGACTTTGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA    | 3180 |
|    |      |  |      |
| Db | 3121 | GAGTGACTTTGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA    | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
|    |      |  |      |
| Db | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 3300 |
|    |      |  |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
|    |      |  |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |

|    |      |   |      |
|----|------|---|------|
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
|    |      |   |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 3540 |
|    |      |   |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 3540 |
| Qy | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
|    |      |   |      |
| Db | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAGTGGCTT  | 3660 |
|    |      |   |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAGTGGCTT  | 3660 |
| Qy | 3661 | TTTAAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT  | 3720 |
|    |      |   |      |
| Db | 3661 | TTTAAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT  | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
|    |      |   |      |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
|    |      |   |      |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
| Qy | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT   | 3900 |
|    |      |   |      |
| Db | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT   | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
|    |      |   |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
|    |      |   |      |
| Db | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
|    |      |   |      |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAAACAACTACCTTATTTTC | 4140 |
|    |      |   |      |
| Db | 4081 | TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAAACAACTACCTTATTTTC | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA  | 4200 |
|    |      |   |      |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA  | 4200 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT  | 4260 |
|    |      |   |      |
| Db | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT  | 4260 |

Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
|||||  
Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 9

ADD18443

ID ADD18443 standard; DNA; 4286 BP.

XX

AC ADD18443;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human prostate cancer diagnosis related DNA sequence SeqID15.

XX

KW prostate tissue; cancer diagnostic; cancer marker; prostate cancer; PCA;  
KW male cancer-related death; serum biomarker; tissue biomarker; cytostatic;  
KW gene therapy; prostate biopsy tissue; AMACR;  
KW alpha-methylacyl-coenzyme A racemase; diagnosing cancer; cell growth;  
KW human; ds.

XX

OS Homo sapiens.

XX

PN WO2003012067-A2.

XX

PD 13-FEB-2003.

XX

PF 02-AUG-2002; 2002WO-US024567.

XX

PR 02-AUG-2001; 2001US-0309581P.

PR 15-NOV-2001; 2001US-0334468P.

PR 01-AUG-2002; 2002US-00210120.

XX

PA (UNMI ) UNIV MICHIGAN.

XX

PI Rubin MA, Chinnaiyan AM, Sreekumar A;

XX

DR WPI; 2003-278396/27.

XX

PT Characterizing prostate tissue comprises providing a prostate tissue  
PT sample from a subject and detecting the presence or absence of expression  
PT of hepsin, pim-1 or EZH2.

XX

PS Disclosure; SEQ ID NO 15; 297pp; English.

XX

CC This invention relates to a novel method of characterising prostate  
CC tissue in a subject and to compositions and methods for cancer  
CC diagnostics, including cancer markers, in particular prostate cancer.  
CC Prostate cancer (PCA) is a leading cause of male cancer-related death.  
CC Additional serum and tissue biomarkers would aid diagnosis. The invention  
CC may provide means of producing compounds with a cytostatic activity or  
CC allow the development of gene therapy. The methods of the invention  
CC useful for characterising prostate tissue in a subject, screening  
CC compounds, characterising inconclusive prostate biopsy tissue in a  
CC subject, detecting AMACR (alpha-methylacyl-coenzyme A racemase)  
CC expression in a bodily fluid, characterising tissue in a subject,  
CC diagnosing cancer in a subject and inhibiting the growth of cells. The

CC present sequence is a DNA sequence which is preferably utilised in the  
CC method of the invention.

XX

SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;

Query Match 99.6%; Score 4284.4; DB 9; Length 4286;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60
        |||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
        |||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
        |||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240
        |||
Db    181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300
        |||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
        |||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
        |||
Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
        |||
Db    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540
        |||
Db    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540

Qy    541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA 600
        |||
Db    541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA 600

Qy    601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660
        |||
Db    601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660

Qy    661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720
        |||
Db    661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720
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|    |      |   |      |
|----|------|---|------|
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG | 780  |
|    |      |   |      |
| Db | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG | 780  |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
|    |      |   |      |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
|    |      |   |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
|    |      |   |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
|    |      |   |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTACAAGACAGCAAAGATTGGTGGCTGTTCACTTTCTAT    | 1080 |
|    |      |   |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTACAAGACAGCAAAGATTGGTGGCTGTTCACTTTCTAT    | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
|    |      |   |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
|    |      |   |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
|    |      |   |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
|    |      |   |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
|    |      |   |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
|    |      |   |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
|    |      |   |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
|    |      |   |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTCACTTTCTTTATATTGGACCGAAGTCATTAA  | 1620 |

|    |      |   |      |
|----|------|---|------|
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTATATTGGACCGAAGTCATTAA       | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT  | 1680 |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT  | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT    | 1740 |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT    | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC   | 2220 |
| Db | 2161 | TTTTGAAAATCATTACACTTTTACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC   | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCAATTCA | 2400 |
| Db | 2341 | CAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCAATTCA | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTCAGGATTATTAAATCTTCTTTTT    | 2460 |

|    |      |  |      |
|----|------|--|------|
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT   | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA   | 2520 |
|    |      |  |      |
| Db | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA   | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
|    |      |  |      |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
|    |      |  |      |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
| Qy | 2641 | GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT    | 2700 |
|    |      |  |      |
| Db | 2641 | GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT    | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
|    |      |  |      |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
|    |      |  |      |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT    | 2880 |
|    |      |  |      |
| Db | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT    | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
|    |      |  |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
|    |      |  |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT | 3060 |
|    |      |  |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
|    |      |  |      |
| Db | 3061 | CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
| Qy | 3121 | GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA  | 3180 |
|    |      |  |      |
| Db | 3121 | GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA  | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
|    |      |  |      |
| Db | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCA   | 3300 |
|    |      |  |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCA   | 3300 |



|    |      |  |      |
|----|------|--|------|
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
|    |      |  |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
|    |      |  |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
|    |      |  |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
| Qy | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
|    |      |  |      |
| Db | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT   | 3660 |
|    |      |  |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT   | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT     | 3720 |
|    |      |  |      |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT     | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT     | 3780 |
|    |      |  |      |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT     | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
|    |      |  |      |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
|    |      |  |      |
| Db | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 3960 |
|    |      |  |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 3960 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT   | 4020 |
|    |      |  |      |
| Db | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT   | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 4080 |
|    |      |  |      |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC      | 4140 |
|    |      |  |      |
| Db | 4081 | TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC      | 4140 |

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 |||  
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 |||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 |||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 10

AAF21288

ID AAF21288 standard; DNA; 13611 BP.

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AC AAF21288;

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DT 14-MAR-2001 (first entry)

XX

DE Human low adenosine antisense oligonucleotide related sequence #2855.

XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;

KW human; airway disorder; bronchoconstriction; lung inflammation;

KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;

KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;

KW respiratory obstruction; pulmonary obstruction; impeded respiration;

KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;

KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;

KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;

KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;

KW cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200062736-A2.

XX

PD 26-OCT-2000.

XX

PF 24-MAR-2000; 2000WO-US008020.

XX

PR 06-APR-1999; 99US-0127958P.

XX

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX

PI Nyce JW;

XX

DR WPI; 2000-679539/66.

XX

PT Low adenosine (A) content antisense oligonucleotides which do not trigger

PT adenosine receptors during metabolism, useful e.g. for treating cancers

PT and respiratory obstructions.

XX

PS Disclosure; Page 1277-1280; 1592pp; English.

XX

CC The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention

XX

SQ Sequence 13611 BP; 3676 A; 3007 C; 3056 G; 3868 T; 0 U; 4 Other;

Query Match 99.6%; Score 4284.4; DB 3; Length 13611;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |      |   |      |
|----|------|---|------|
| Qy | 1    | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60   |
|    |      |   |      |
| Db | 1873 | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 1932 |
| Qy | 61   | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120  |
|    |      |   |      |
| Db | 1933 | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 1992 |
| Qy | 121  | AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA  | 180  |
|    |      |   |      |
| Db | 1993 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA  | 2052 |
| Qy | 181  | AACTTGGCTCTGAAACTGCGGACGCGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240  |
|    |      |   |      |
| Db | 2053 | AACTTGGCTCTGAAACTGCGGACGCGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 2112 |
| Qy | 241  | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300  |
|    |      |   |      |
| Db | 2113 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 2172 |
| Qy | 301  | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360  |

|    |      |  |      |
|----|------|--|------|
| Db | 2173 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA   | 2232 |
| Qy | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 420  |
| Db | 2233 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 2292 |
| Qy | 421  | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG  | 480  |
| Db | 2293 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG  | 2352 |
| Qy | 481  | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540  |
| Db | 2353 | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 2412 |
| Qy | 541  | TACATCAACACGGTTGTGTCCTGCCTTGTGTTCGTGCTGGGGATCATCGGGAACCTCCACA  | 600  |
| Db | 2413 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTCGTGCTGGGGATCATCGGGAACCTCCACA  | 2472 |
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Db | 2473 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 2532 |
| Qy | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Db | 2533 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 2592 |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Db | 2593 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 2652 |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Db | 2653 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 2712 |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Db | 2713 | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 2772 |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
| Db | 2773 | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 2832 |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG  | 1020 |
| Db | 2833 | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG  | 2892 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Db | 2893 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 2952 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Db | 2953 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 3012 |
| Qy | 1141 | AGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |

|    |      |   |      |
|----|------|---|------|
| Db | 3013 | AGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG | 3072 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
|    |      |   |      |
| Db | 3073 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 3132 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
|    |      |   |      |
| Db | 3133 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 3192 |
| Qy | 1321 | AGCTTCTGTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT    | 1380 |
|    |      |   |      |
| Db | 3193 | AGCTTCTGTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT    | 3252 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
|    |      |   |      |
| Db | 3253 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 3312 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
|    |      |   |      |
| Db | 3313 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 3372 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
|    |      |   |      |
| Db | 3373 | AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA  | 3432 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACCGAAGTCATTAA       | 1620 |
|    |      |   |      |
| Db | 3433 | TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACCGAAGTCATTAA       | 3492 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
|    |      |   |      |
| Db | 3493 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT   | 3552 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT    | 1740 |
|    |      |   |      |
| Db | 3553 | TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT    | 3612 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 3613 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 3672 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 3673 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 3732 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
|    |      |   |      |
| Db | 3733 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 3792 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
|    |      |   |      |
| Db | 3793 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 3852 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
|    |      |   |      |
| Db | 3853 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 3912 |

|    |      |   |      |
|----|------|---|------|
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 3913 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 3972 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAGAGCAAGGCTGT | 2160 |
|    |      |   |      |
| Db | 3973 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAGAGCAAGGCTGT | 4032 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
|    |      |   |      |
| Db | 4033 | TTTTGAAAATCATTACACTTTCACTAGAAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 4092 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
|    |      |   |      |
| Db | 4093 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 4152 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAGTTAAGATCAAACCTCA  | 2340 |
|    |      |   |      |
| Db | 4153 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAGTTAAGATCAAACCTCA  | 4212 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA  | 2400 |
|    |      |   |      |
| Db | 4213 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA  | 4272 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 2460 |
|    |      |   |      |
| Db | 4273 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 4332 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
|    |      |   |      |
| Db | 4333 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 4392 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
|    |      |   |      |
| Db | 4393 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 4452 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
|    |      |   |      |
| Db | 4453 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 4512 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT  | 2700 |
|    |      |   |      |
| Db | 4513 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT  | 4572 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
|    |      |   |      |
| Db | 4573 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 4632 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
|    |      |   |      |
| Db | 4633 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 4692 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT  | 2880 |
|    |      |   |      |
| Db | 4693 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT  | 4752 |

|    |      |  |      |
|----|------|--|------|
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
|    |      |  |      |
| Db | 4753 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 4812 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
|    |      |  |      |
| Db | 4813 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 4872 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
|    |      |  |      |
| Db | 4873 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTTCGTCATTGCCT | 4932 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
|    |      |  |      |
| Db | 4933 | CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 4992 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA   | 3180 |
|    |      |  |      |
| Db | 4993 | GAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA   | 5052 |
| Qy | 3181 | ATTTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG     | 3240 |
|    |      |  |      |
| Db | 5053 | ATTTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG     | 5112 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 3300 |
|    |      |  |      |
| Db | 5113 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 5172 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
|    |      |  |      |
| Db | 5173 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 5232 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 5233 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 5292 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTACAGTTTATTAA     | 3480 |
|    |      |  |      |
| Db | 5293 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTACAGTTTATTAA     | 5352 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
|    |      |  |      |
| Db | 5353 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 5412 |
| Qy | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
|    |      |  |      |
| Db | 5413 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 5472 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT  | 3660 |
|    |      |  |      |
| Db | 5473 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT  | 5532 |
| Qy | 3661 | TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
|    |      |  |      |
| Db | 5533 | TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 5592 |
| Qy | 3721 | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT   | 3780 |

|    |      |  |      |
|----|------|--|------|
| Db | 5593 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT     | 5652 |
| Qy | 3781 | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
| Db | 5653 | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 5712 |
| Qy | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
| Db | 5713 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT    | 5772 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 3960 |
| Db | 5773 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 5832 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAAGTGTAATATAACAATGT  | 4020 |
| Db | 5833 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAAGTGTAATATAACAATGT  | 5892 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 4080 |
| Db | 5893 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 5952 |
| Qy | 4081 | TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTC | 4140 |
| Db | 5953 | TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTC | 6012 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA   | 4200 |
| Db | 6013 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA   | 6072 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT   | 4260 |
| Db | 6073 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT   | 6132 |
| Qy | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                     | 4286 |
| Db | 6133 | AAAATGCCACATTTCTGGTCTCTGGG                                     | 6158 |

RESULT 11

ABZ96982

ID ABZ96982 standard; DNA; 13611 BP.

XX

AC ABZ96982;

XX

DT 17-OCT-2003 (first entry)

XX

DE Human nucleic acid sequence.

XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX





Db 1933 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 1992  
 Qy 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1993 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 2052  
 Qy 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||  
 Db 2053 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 2112  
 Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300  
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||  
 Db 2113 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 2172  
 Qy 301 TCGCGGATCTGGGGAGAGGAGAGAGAGGCTTCCCGCCTGACAGGGGCACTCCGCTTTTGCAA 360  
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||  
 Db 2173 TCGCGGATCTGGGGAGAGGAGAGAGAGGCTTCCCGCCTGACAGGGGCACTCCGCTTTTGCAA 2232  
 Qy 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420  
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||  
 Db 2233 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 2292  
 Qy 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||  
 Db 2293 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 2352  
 Qy 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540  
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||  
 Db 2353 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 2412  
 Qy 541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA 600  
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||  
 Db 2413 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA 2472  
 Qy 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||  
 Db 2473 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 2532  
 Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||  
 Db 2533 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 2592  
 Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 780  
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||  
 Db 2593 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 2652  
 Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||  
 Db 2653 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 2712  
 Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||  
 Db 2713 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 2772  
 Qy 901 ATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||  
 Db 2773 ATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 2832

|    |      |  |      |
|----|------|--|------|
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG | 1020 |
|    |      |  |      |
| Db | 2833 | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG | 2892 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
|    |      |  |      |
| Db | 2893 | AAGACAGCTTTCATGCAGTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 2952 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG | 1140 |
|    |      |  |      |
| Db | 2953 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG | 3012 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG | 1200 |
|    |      |  |      |
| Db | 3013 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG | 3072 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
|    |      |  |      |
| Db | 3073 | GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 3132 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG | 1320 |
|    |      |  |      |
| Db | 3133 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG | 3192 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT | 1380 |
|    |      |  |      |
| Db | 3193 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT | 3252 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA  | 1440 |
|    |      |  |      |
| Db | 3253 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA  | 3312 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA | 1500 |
|    |      |  |      |
| Db | 3313 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA | 3372 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA | 1560 |
|    |      |  |      |
| Db | 3373 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA | 3432 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA     | 1620 |
|    |      |  |      |
| Db | 3433 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA     | 3492 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT | 1680 |
|    |      |  |      |
| Db | 3493 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT | 3552 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT | 1740 |
|    |      |  |      |
| Db | 3553 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT | 3612 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT | 1800 |
|    |      |  |      |
| Db | 3613 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT | 3672 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 3673 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 3732 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
|    |      |   |      |
| Db | 3733 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 3792 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
|    |      |   |      |
| Db | 3793 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 3852 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
|    |      |   |      |
| Db | 3853 | AAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAAACAACCTTTTCAATTAATAT | 3912 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 3913 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 3972 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
|    |      |   |      |
| Db | 3973 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 4032 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTCACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
|    |      |   |      |
| Db | 4033 | TTTTGAAAATCATTACACTTTTCACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 4092 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
|    |      |   |      |
| Db | 4093 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 4152 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAGTTAAGATCAAACCTCA  | 2340 |
|    |      |   |      |
| Db | 4153 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAGTTAAGATCAAACCTCA  | 4212 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA  | 2400 |
|    |      |   |      |
| Db | 4213 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA  | 4272 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTTT   | 2460 |
|    |      |   |      |
| Db | 4273 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTTT   | 4332 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
|    |      |   |      |
| Db | 4333 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 4392 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
|    |      |   |      |
| Db | 4393 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 4452 |
| Qy | 2581 | GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
|    |      |   |      |
| Db | 4453 | GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 4512 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT  | 2700 |

|    |      |  |      |
|----|------|--|------|
| Db | 4513 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 4572 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG    | 2760 |
| Db | 4573 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG    | 4632 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
| Db | 4633 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 4692 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCCAAACTGCTTTTTGAGACCGTAAGAACCTCTT   | 2880 |
| Db | 4693 | ACATGGTGCTTTTCTTTCATCTAGAGGCCAAACTGCTTTTTGAGACCGTAAGAACCTCTT   | 4752 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCCTAGGATAGCTT   | 2940 |
| Db | 4753 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCCTAGGATAGCTT   | 4812 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
| Db | 4813 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 4872 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
| Db | 4873 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 4932 |
| Qy | 3061 | CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAACACAGTGCAATGTTCTCA      | 3120 |
| Db | 4933 | CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAACACAGTGCAATGTTCTCA      | 4992 |
| Qy | 3121 | GAGTGACTTTGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA     | 3180 |
| Db | 4993 | GAGTGACTTTGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA     | 5052 |
| Qy | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
| Db | 5053 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 5112 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 3300 |
| Db | 5113 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 5172 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Db | 5173 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 5232 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Db | 5233 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 5292 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Db | 5293 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 5352 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |

Db 5353 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA 5412

Qy 3541 TCCTGATACCCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 |||

Db 5413 TCCTGATACCCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 5472

Qy 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAAGTGGCTT 3660  
 |||

Db 5473 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAAGTGGCTT 5532

Qy 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 |||

Db 5533 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 5592

Qy 3721 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780  
 |||

Db 5593 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT 5652

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 |||

Db 5653 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 5712

Qy 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 |||

Db 5713 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 5772

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 |||

Db 5773 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 5832

Qy 3961 GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 |||

Db 5833 GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 5892

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 |||

Db 5893 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 5952

Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 4140  
 |||

Db 5953 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 6012

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200  
 |||

Db 6013 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 6072

Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 |||

Db 6073 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 6132

Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 |||

Db 6133 AAAATGCCACATTTCTGGTCTCTGGG 6158

ID AAA35166 standard; DNA; 13612 BP.  
XX  
AC AAA35166;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:40.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US017712.  
XX  
PR 03-AUG-1998; 98US-0095212P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-205971/18.  
XX  
PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
PS Disclosure; Page 1194-1197; 1343pp; English.  
XX  
CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the

CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing

XX

SQ Sequence 13612 BP; 3677 A; 3007 C; 3056 G; 3868 T; 0 U; 4 Other;

Query Match 99.6%; Score 4284.4; DB 3; Length 13612;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |      |   |      |
|----|------|---|------|
| Qy | 1    | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC   | 60   |
|    |      |   |      |
| Db | 1873 | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC   | 1932 |
| Qy | 61   | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120  |
|    |      |   |      |
| Db | 1933 | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 1992 |
| Qy | 121  | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACCTGGTACTTGGAGTCTGGACATCTGA | 180  |
|    |      |   |      |
| Db | 1993 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACCTGGTACTTGGAGTCTGGACATCTGA | 2052 |
| Qy | 181  | AACCTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240  |
|    |      |   |      |
| Db | 2053 | AACCTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 2112 |
| Qy | 241  | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300  |
|    |      |   |      |
| Db | 2113 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 2172 |
| Qy | 301  | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360  |
|    |      |   |      |
| Db | 2173 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 2232 |
| Qy | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420  |
|    |      |   |      |
| Db | 2233 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 2292 |
| Qy | 421  | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480  |
|    |      |   |      |
| Db | 2293 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 2352 |
| Qy | 481  | CCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA   | 540  |
|    |      |   |      |
| Db | 2353 | CCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA   | 2412 |
| Qy | 541  | TACATCAACACGGTTGTGTCTGCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCACA   | 600  |
|    |      |   |      |
| Db | 2413 | TACATCAACACGGTTGTGTCTGCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCACA   | 2472 |
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660  |
|    |      |   |      |



|    |      |  |      |
|----|------|--|------|
| Db | 2473 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 2532 |
| Qy | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
|    |      |  |      |
| Db | 2533 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 2592 |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
|    |      |  |      |
| Db | 2593 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 2652 |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
|    |      |  |      |
| Db | 2653 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 2712 |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
|    |      |  |      |
| Db | 2713 | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 2772 |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
|    |      |  |      |
| Db | 2773 | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 2832 |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
|    |      |  |      |
| Db | 2833 | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 2892 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
|    |      |  |      |
| Db | 2893 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 2952 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
|    |      |  |      |
| Db | 2953 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 3012 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
|    |      |  |      |
| Db | 3013 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 3072 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
|    |      |  |      |
| Db | 3073 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 3132 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
|    |      |  |      |
| Db | 3133 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 3192 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
|    |      |  |      |
| Db | 3193 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 3252 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
|    |      |  |      |
| Db | 3253 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 3312 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
|    |      |  |      |
| Db | 3313 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 3372 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAAATACAGCTCA | 1560 |
|    |      |   |      |
| Db | 3373 | AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAAATACAGCTCA | 3432 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTATATTGGACCGAAGTCATTAA       | 1620 |
|    |      |   |      |
| Db | 3433 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTATATTGGACCGAAGTCATTAA       | 3492 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT   | 1680 |
|    |      |   |      |
| Db | 3493 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT   | 3552 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
|    |      |   |      |
| Db | 3553 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 3612 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 3613 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 3672 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 3673 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 3732 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA  | 1920 |
|    |      |   |      |
| Db | 3733 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA  | 3792 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
|    |      |   |      |
| Db | 3793 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 3852 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
|    |      |   |      |
| Db | 3853 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 3912 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 3913 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 3972 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
|    |      |   |      |
| Db | 3973 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 4032 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
|    |      |   |      |
| Db | 4033 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 4092 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
|    |      |   |      |
| Db | 4093 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 4152 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA | 2340 |
|    |      |   |      |
| Db | 4153 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA | 4212 |

|    |      |   |      |
|----|------|---|------|
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA  | 2400 |
|    |      |   |      |
| Db | 4213 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA  | 4272 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 2460 |
|    |      |   |      |
| Db | 4273 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 4332 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
|    |      |   |      |
| Db | 4333 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 4392 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
|    |      |   |      |
| Db | 4393 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 4452 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
|    |      |   |      |
| Db | 4453 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 4512 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 2700 |
|    |      |   |      |
| Db | 4513 | GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 4572 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
|    |      |   |      |
| Db | 4573 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 4632 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
|    |      |   |      |
| Db | 4633 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 4692 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT   | 2880 |
|    |      |   |      |
| Db | 4693 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT   | 4752 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT | 2940 |
|    |      |   |      |
| Db | 4753 | AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT | 4812 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
|    |      |   |      |
| Db | 4813 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 4872 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
|    |      |   |      |
| Db | 4873 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 4932 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |
|    |      |   |      |
| Db | 4933 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 4992 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA | 3180 |
|    |      |   |      |
| Db | 4993 | GAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA | 5052 |
| Qy | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG  | 3240 |

|    |      |   |      |
|----|------|---|------|
| Db | 5053 | <br>ATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 5112 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA        | 3300 |
| Db | 5113 | <br>TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA    | 5172 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC      | 3360 |
| Db | 5173 | <br>GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 5232 |
| Qy | 3361 | ACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT     | 3420 |
| Db | 5233 | <br>ACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 5292 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA      | 3480 |
| Db | 5293 | <br>CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 5352 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA        | 3540 |
| Db | 5353 | <br>TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 5412 |
| Qy | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT      | 3600 |
| Db | 5413 | <br>TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 5472 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT      | 3660 |
| Db | 5473 | <br>TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT  | 5532 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT       | 3720 |
| Db | 5533 | <br>TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 5592 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT        | 3780 |
| Db | 5593 | <br>TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 5652 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA      | 3840 |
| Db | 5653 | <br>TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 5712 |
| Qy | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT       | 3900 |
| Db | 5713 | <br>CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT   | 5772 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA      | 3960 |
| Db | 5773 | <br>GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 5832 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT      | 4020 |
| Db | 5833 | <br>GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 5892 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGTTGCCTAAAGTGGCTATAGTTACTGATTT       | 4080 |
|    |      |   |      |

Db 5893 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 5952  
 Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140  
 Db 5953 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 6012  
 Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 Db 6013 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 6072  
 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 Db 6073 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 6132  
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 Db 6133 AAAATGCCACATTTCTGGTCTCTGGG 6158

RESULT 13

ACH03911

ID ACH03911 standard; cDNA; 4305 BP.

XX

AC ACH03911;

XX

DT 26-SEP-2003 (first entry)

XX

DE Human cDNA differentially expressed in lung cancer #116.

XX

KW Gene therapy; emphysema; ss; gene; chronic obstructive pulmonary disease;  
 KW respiratory disorder; lung cancer; asthma; human.

XX

OS Homo sapiens.

XX

PN US2003065157-A1.

XX

PD 03-APR-2003.

XX

PF 04-APR-2002; 2002US-00116802.

XX

PR 04-APR-2001; 2001US-0281593P.

XX

PA (LASE/) LASEK A W.

XX

PI Lasek AW;

XX

DR WPI; 2003-540803/51.

XX

PT New combination comprising cDNAs that are differentially expressed in  
 PT respiratory disorders, useful for diagnosing or treating respiratory  
 PT disorders e.g., lung cancer, chronic obstructive pulmonary disease,  
 PT emphysema or asthma.

XX

PS Claim 1; Page; 39pp; English.

XX

CC The invention relates to a combination comprising cDNAs or their  
 CC complements that are differentially expressed in respiratory disorder.

CC The combination is useful for preparing a composition for diagnosing or  
CC treating respiratory disorders e.g. lung cancer, chronic obstructive  
CC pulmonary disease, emphysema or asthma. The present sequence represents  
CC human cDNA differentially expressed during lung cancer  
XX  
SQ Sequence 4305 BP; 1341 A; 835 C; 816 G; 1311 T; 0 U; 2 Other;

Query Match 97.7%; Score 4202.4; DB 8; Length 4305;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 4280; Conservative 0; Mismatches 18; Indels 8; Gaps 6;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGAGTCTGGACATCTGA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540

Qy    541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAGTCCACA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAGTCCACA 600

Qy    601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660

Qy    661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
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|    |      |  |      |
|----|------|--|------|
| Db | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
|    |      |  |      |
| Db | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
|    |      |  |      |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
|    |      |  |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGTTTTGAT    | 960  |
|    |      |  |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGTTTTGAT    | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG  | 1020 |
|    |      |  |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
|    |      |  |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
|    |      |  |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
|    |      |  |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
|    |      |  |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
|    |      |  |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
|    |      |  |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
|    |      |  |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
|    |      |  |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
|    |      |   |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTGTCACAGCACACTAT  | 1680 |
|    |      |   |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTGTCACAGCACACTAT  | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
|    |      |   |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA  | 1920 |
|    |      |   |      |
| Db | 1861 | TAGGCTTAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA  | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
|    |      |   |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
|    |      |   |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
|    |      |   |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCAC--TAGAAGCCCCAACCTCAGCATT-CTGCAATATGT  | 2217 |
|    |      |   |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTCACCTAGAAGCCCCAACCTCAGCATTCTGCAATATGT    | 2220 |
| Qy | 2218 | AA-CCAACATGTCACAAACAAGCAG--CATGTAACAGACTGGCACATGTG-CCAGCTGAA  | 2273 |
|    |      |   |      |
| Db | 2221 | AACCCAACATGTCACAAACAAGCCAGCCATGTAACAGACTGGCACATGTGCCAGCTGAA   | 2280 |
| Qy | 2274 | TTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCA   | 2333 |
|    |      |   |      |
| Db | 2281 | TTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCA   | 2340 |
| Qy | 2334 | AACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTG   | 2393 |
|    |      |   |      |
| Db | 2341 | AACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTG   | 2400 |



|    |      |   |      |
|----|------|---|------|
| Qy | 2394 | TCATTCACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCT  | 2453 |
|    |      |   |      |
| Db | 2401 | TCATTCACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCT  | 2460 |
| Qy | 2454 | TCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCT  | 2513 |
|    |      |   |      |
| Db | 2461 | TCTTCTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCT   | 2520 |
| Qy | 2514 | ACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATG  | 2573 |
|    |      |   |      |
| Db | 2521 | ACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATG  | 2580 |
| Qy | 2574 | GAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGA  | 2633 |
|    |      |   |      |
| Db | 2581 | GAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGA  | 2640 |
| Qy | 2634 | CAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATAT | 2693 |
|    |      |   |      |
| Db | 2641 | CAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATAT | 2700 |
| Qy | 2694 | GTATAATGCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAG | 2753 |
|    |      |   |      |
| Db | 2701 | GTATAATGCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAG | 2760 |
| Qy | 2754 | CTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGT  | 2813 |
|    |      |   |      |
| Db | 2761 | CTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGT  | 2820 |
| Qy | 2814 | TTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGA   | 2873 |
|    |      |   |      |
| Db | 2821 | TTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGA   | 2880 |
| Qy | 2874 | ACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGG  | 2933 |
|    |      |   |      |
| Db | 2881 | ACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGG  | 2940 |
| Qy | 2934 | ATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAA  | 2993 |
|    |      |   |      |
| Db | 2941 | ATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAA  | 3000 |
| Qy | 2994 | TGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTC | 3053 |
|    |      |   |      |
| Db | 3001 | TGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTC | 3060 |
| Qy | 3054 | ATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAAT     | 3113 |
|    |      |   |      |
| Db | 3061 | ATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAAT     | 3120 |
| Qy | 3114 | GTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATA   | 3173 |
|    |      |   |      |
| Db | 3121 | GTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATA   | 3180 |
| Qy | 3174 | TGCCCAAATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCT    | 3233 |
|    |      |   |      |
| Db | 3181 | TGCCCAAATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCT    | 3240 |
| Qy | 3234 | AGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAAT   | 3293 |

|    |      |   |      |
|----|------|---|------|
| Db | 3241 | <br>AGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAAT  | 3300 |
| Qy | 3294 | GTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAA      | 3353 |
| Db | 3301 | <br>GTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAA  | 3360 |
| Qy | 3354 | ATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCA     | 3413 |
| Db | 3361 | <br>ATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCA | 3420 |
| Qy | 3414 | TAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGT      | 3473 |
| Db | 3421 | <br>TAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGT  | 3480 |
| Qy | 3474 | TTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAAT       | 3533 |
| Db | 3481 | <br>TTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAAT   | 3540 |
| Qy | 3534 | TTTTACATCCTGATACCCCTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGC      | 3593 |
| Db | 3541 | <br>TTTTACATCCTGATACCCCTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGC  | 3600 |
| Qy | 3594 | CAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCA      | 3653 |
| Db | 3601 | <br>CAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCA  | 3660 |
| Qy | 3654 | GTGGCTTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAA       | 3713 |
| Db | 3661 | <br>GTGGCTTTTTT-AAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAA  | 3719 |
| Qy | 3714 | TTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAA       | 3773 |
| Db | 3720 | <br>TTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAA   | 3779 |
| Qy | 3774 | AACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATG      | 3833 |
| Db | 3780 | <br>AACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATG  | 3839 |
| Qy | 3834 | GATGTTACAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCAC        | 3893 |
| Db | 3840 | <br>GATGTTACAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCAC    | 3899 |
| Qy | 3894 | TGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAG      | 3953 |
| Db | 3900 | <br>TGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAG  | 3959 |
| Qy | 3954 | GAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATA      | 4013 |
| Db | 3960 | <br>GAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATA  | 4019 |
| Qy | 4014 | ACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTA      | 4073 |
| Db | 4020 | <br>ACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTA  | 4079 |
| Qy | 4074 | CTGATTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTT        | 4133 |
|    |      |   |      |

Db 4080 CTGATTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTT 4139  
 QY 4134 ATTTTTCACACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATA 4193  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4140 ATTTTTCACACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATA 4199  
 QY 4194 AATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTA 4253  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4200 AATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTA 4259  
 QY 4254 TTCAATTAAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAA 4299  
 |||||||||||||||||||||||| ||||| |  
 Db 4260 TTCAATTAAAATGCCACATTTCTGGTCAAAAAAAAAAAAAAGNNAGA 4305

RESULT 14

ABK94410

ID ABK94410 standard; DNA; 2972 BP.

XX

AC ABK94410;

XX

DT 27-AUG-2002 (first entry)

XX

DE DNA encoding endothelin receptor B (EDNRB), exon 7.

XX

KW Endothelin; EDN; endothelin converting enzyme; ECE; EDNRB;

KW endothelin receptor B; signaling system; cardiovascular disease;

KW coronary heart disease; hypertension; atherosclerosis; angiogenesis;

KW fatty acid metabolism; diabetes; familial hypercholesterolaemia;

KW forensic marker; transgenic animal; solid support; SNP;

KW cardiovascular regulator; gene; ds; single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT variation replace(1048,A)

FT /\*tag= a

FT /standard\_name= "Single nucleotide polymorphism"

FT variation replace(1658,C)

FT /\*tag= b

FT /standard\_name= "Single nucleotide polymorphism"

FT variation replace(1912,T)

FT /\*tag= c

FT /standard\_name= "Single nucleotide polymorphism"

FT variation replace(2130,T)

FT /\*tag= d

FT /standard\_name= "Single nucleotide polymorphism"

XX

PN WO200224747-A2.

XX

PD 28-MAR-2002.

XX

PF 31-AUG-2001; 2001WO-EP010087.

XX

PR 19-SEP-2000; 2000EP-00120123.

XX

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX  
PI Brinkmann U, Hoffmeyer S;  
XX  
DR WPI; 2002-435060/46.  
XX  
PT Novel polynucleotide of the endothelin/endothelin converting  
PT enzyme/receptors of endothelin and endothelin converting enzyme signaling  
PT system associated with cardiovascular disease, useful for treating the  
PT disease.  
XX  
PS Claim 1; Page; 190pp; English.  
XX  
CC The invention describes a polynucleotide (I) of the endothelin  
CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)  
CC signaling system which is associated with a cardiovascular disease. (I),  
CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)  
CC or (II) is useful for producing cells capable of expressing a molecular  
CC variant polypeptide which is associated with a cardiovascular disease.  
CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a  
CC molecular variant gene comprising (I) is useful for identifying and  
CC obtaining a pro-drug or drug capable of modulating the activity of a  
CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system  
CC or its gene product, or for identifying and obtaining an inhibitor of the  
CC activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE  
CC signaling system or its gene product. The isolated proteins and  
CC polynucleotides encoding them are useful for preparation of a  
CC pharmaceutical composition for treating a cardiovascular disease such as  
CC coronary heart disease, hypertension, atherosclerosis, or related to  
CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial  
CC hypercholesterolaemia. The gene or a polynucleotide fragment of the  
CC EDN/ECE/EDNR signaling system are useful as forensic markers, for  
CC creating a transgenic animal and in creation of a solid support  
CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or  
CC host cells of the invention. This sequence encodes a fragment of the  
CC cardioavscular regulator Endothelin receptor B (EDNRB). Note: This  
CC sequence does not appear in the specification but has been obtained from  
CC GenBank using information given in the invention  
XX  
SQ Sequence 2972 BP; 1018 A; 499 C; 465 G; 990 T; 0 U; 0 Other;

|    |      |   |      |
|----|------|---|------|
| Db | 189  | GAAGTCATTAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA  | 248  |
| Qy | 1670 | CAGCACACTATTAAAATATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATT | 1729 |
| Db | 249  | CAGCACACTATTAAAATATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATT | 308  |
| Qy | 1730 | TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA  | 1789 |
| Db | 309  | TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA  | 368  |
| Qy | 1790 | AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATT  | 1849 |
| Db | 369  | AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATT  | 428  |
| Qy | 1850 | CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG  | 1909 |
| Db | 429  | CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG  | 488  |
| Qy | 1910 | ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA  | 1969 |
| Db | 489  | ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA  | 548  |
| Qy | 1970 | ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTT | 2029 |
| Db | 549  | ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTT | 608  |
| Qy | 2030 | TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT  | 2089 |
| Db | 609  | TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT  | 668  |
| Qy | 2090 | AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAG | 2149 |
| Db | 669  | AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAG | 728  |
| Qy | 2150 | AGCAAGGCTGTTTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTG  | 2209 |
| Db | 729  | AGCAAGGCTGTTTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTG  | 788  |
| Qy | 2210 | CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC  | 2269 |
| Db | 789  | CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC  | 848  |
| Qy | 2270 | TGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTTAAG | 2329 |
| Db | 849  | TGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTTAAG | 908  |
| Qy | 2330 | ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA   | 2389 |
| Db | 909  | ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA   | 968  |
| Qy | 2390 | TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAA  | 2449 |
| Db | 969  | TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAA  | 1028 |
| Qy | 2450 | ATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT  | 2509 |

|    |      |   |      |
|----|------|---|------|
| Db | 1029 | ATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT  | 1088 |
| Qy | 2510 | ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC  | 2569 |
|    |      |   |      |
| Db | 1089 | ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC  | 1148 |
| Qy | 2570 | GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC  | 2629 |
|    |      |   |      |
| Db | 1149 | GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC  | 1208 |
| Qy | 2630 | ATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGC | 2689 |
|    |      |   |      |
| Db | 1209 | ATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGC | 1268 |
| Qy | 2690 | ATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTA | 2749 |
|    |      |   |      |
| Db | 1269 | ATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTA | 1328 |
| Qy | 2750 | ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA  | 2809 |
|    |      |   |      |
| Db | 1329 | ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA  | 1388 |
| Qy | 2810 | AAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT  | 2869 |
|    |      |   |      |
| Db | 1389 | AAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT  | 1448 |
| Qy | 2870 | AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCT  | 2929 |
|    |      |   |      |
| Db | 1449 | AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCT  | 1508 |
| Qy | 2930 | TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG  | 2989 |
|    |      |   |      |
| Db | 1509 | TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG  | 1568 |
| Qy | 2990 | GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCTTAGCCTAACGTT       | 3049 |
|    |      |   |      |
| Db | 1569 | GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCTTAGCCTAACGTT       | 1628 |
| Qy | 3050 | CGTCATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTG     | 3109 |
|    |      |   |      |
| Db | 1629 | CGTCATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTG     | 1688 |
| Qy | 3110 | CAATGTTCTCAGAGTGACTTTTGGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA | 3169 |
|    |      |   |      |
| Db | 1689 | CAATGTTCTCAGAGTGACTTTTGGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA | 1748 |
| Qy | 3170 | AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA  | 3229 |
|    |      |   |      |
| Db | 1749 | AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA  | 1808 |
| Qy | 3230 | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA   | 3289 |
|    |      |   |      |
| Db | 1809 | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA   | 1868 |
| Qy | 3290 | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT  | 3349 |
|    |      |   |      |
| Db | 1869 | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT  | 1928 |

|    |      |  |      |
|----|------|--|------|
| Qy | 3350 | ATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT | 3409 |
|    |      |  |      |
| Db | 1929 | ATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT | 1988 |
| Qy | 3410 | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA   | 3469 |
|    |      |  |      |
| Db | 1989 | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA   | 2048 |
| Qy | 3470 | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT   | 3529 |
|    |      |  |      |
| Db | 2049 | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT   | 2108 |
| Qy | 3530 | GAATTTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC   | 3589 |
|    |      |  |      |
| Db | 2109 | GAATTTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC   | 2168 |
| Qy | 3590 | TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA   | 3649 |
|    |      |  |      |
| Db | 2169 | TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA   | 2228 |
| Qy | 3650 | TTCAGTGGCTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA     | 3709 |
|    |      |  |      |
| Db | 2229 | TTCAGTGGCTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA     | 2288 |
| Qy | 3710 | ACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT    | 3769 |
|    |      |  |      |
| Db | 2289 | ACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT    | 2348 |
| Qy | 3770 | TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA   | 3829 |
|    |      |  |      |
| Db | 2349 | TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA   | 2408 |
| Qy | 3830 | CATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT    | 3889 |
|    |      |  |      |
| Db | 2409 | CATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT    | 2468 |
| Qy | 3890 | CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC   | 3949 |
|    |      |  |      |
| Db | 2469 | CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC   | 2528 |
| Qy | 3950 | AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA    | 4009 |
|    |      |  |      |
| Db | 2529 | AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA    | 2588 |
| Qy | 4010 | TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA   | 4069 |
|    |      |  |      |
| Db | 2589 | TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA   | 2648 |
| Qy | 4070 | GTTACTGATTTTTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTA       | 4129 |
|    |      |  |      |
| Db | 2649 | GTTACTGATTTTTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTA       | 2708 |
| Qy | 4130 | CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAA   | 4189 |
|    |      |  |      |
| Db | 2709 | CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAA   | 2768 |

QY 4190 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 4249  
 |||  
 Db 2769 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 2828  
 QY 4250 GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 4286  
 |||  
 Db 2829 GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 2865

RESULT 15

ABQ77402/c

ID ABQ77402 standard; DNA; 183337 BP.

XX

AC ABQ77402;

XX

DT 10-MAY-2003 (first entry)

XX

DE Human EDNRB DNA.

XX

KW Human; EDNRB; vascular disease; cardiant; antiarteriosclerotic; stroke;

KW cerebroprotective; gene therapy; coronary artery disease; ischaemia;

KW myocardial infarction; peripheral vascular disease; pulmonary embolism;

KW venous thromboembolism; forensic; paternity testing; GI12597038; gene;

KW SNP; single nucleotide polymorphism; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT variation replace(75672,t)

FT /\*tag= a

FT /standard\_name= "SNP"

FT /note= "Single nucleotide polymorphism (ID G337a4) which  
 FT does not change the EDNRB protein"

XX

PN WO2003016494-A2.

XX

PD 27-FEB-2003.

XX

PF 16-AUG-2002; 2002WO-US026343.

XX

PR 16-AUG-2001; 2001US-0313097P.

PR 05-OCT-2001; 2001US-0327485P.

PR 14-DEC-2001; 2001US-00020141.

XX

PA (VITI-) VITIVITY INC.

XX

PI Mccarthy J, Ableson A;

XX

DR WPI; 2003-300617/29.

DR P-PSDB; ABG74670.

XX

PT Identifying a subject as a candidate for a particular course of therapy

PT to treat a vascular disease or disorder, e.g. stroke, myocardial

PT infarction or ischemia by determining the identity of the nucleotide

PT present at specific positions.

XX

PS Claim 1; Fig 5; 568pp; English.



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XX
CC   This invention describes a novel method for identifying a subject as a
CC   candidate for a particular course of therapy to treat a vascular disease
CC   or disorder. The method comprises determining the identity of the
CC   nucleotide present at specific positions, or their complements, and
CC   identifying the subject as a candidate for a particular clinical course
CC   of therapy based on the identity of the nucleotide present in that
CC   specific position. The method can be used for identifying a subject who
CC   is a candidate for further diagnostic evaluation of a vascular disease or
CC   disorder and selecting a clinical course of therapy. The products of the
CC   invention have cardiant, antiarteriosclerotic and cerebroprotective
CC   activity and can be used for gene therapy. The methods disclosed are
CC   useful for treating a vascular disease, e.g. atherosclerosis, coronary
CC   artery disease, myocardial infarction, ischaemia, stroke, peripheral
CC   vascular diseases, venous thromboembolism and pulmonary embolism. The DNA
CC   sequences are useful as fingerprint for detecting different individuals
CC   within the same species applicable in forensic studies and paternity
CC   testing. This sequence encodes the human EDNBR gene represented in
CC   GI12597038, used to illustrate the method of the invention
XX
SQ   Sequence 183337 BP; 56451 A; 33595 C; 34663 G; 58628 T; 0 U; 0 Other;

Query Match          66.1%;  Score 2841.8;  DB 7;  Length 183337;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 2854;  Conservative 0;  Mismatches 2;  Indels 1;  Gaps 1;

Qy      1430 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 1489
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72830 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 72771

Qy      1490 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 1549
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72770 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 72711

Qy      1550 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACC 1609
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72710 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACC 72651

Qy      1610 GAAGTCATTAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA 1669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72650 GAAGTCATTAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA 72591

Qy      1670 CAGCACACTATTAAATATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATT 1729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72590 CAGCACACTATTAAATATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATT 72531

Qy      1730 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA 1789
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72530 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA 72471

Qy      1790 AAGCACTTAATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT 1849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72470 AAGCACTTAATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT 72411

Qy      1850 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG 1909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72410 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG 72351

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|    |       |  |       |
|----|-------|--|-------|
| Qy | 1910  | ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA   | 1969  |
|    |       |  |       |
| Db | 72350 | ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA   | 72291 |
| Qy | 1970  | ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACTTT   | 2029  |
|    |       |  |       |
| Db | 72290 | ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACTTT   | 72231 |
| Qy | 2030  | TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT   | 2089  |
|    |       |  |       |
| Db | 72230 | TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT   | 72171 |
| Qy | 2090  | AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG | 2149  |
|    |       |  |       |
| Db | 72170 | AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG | 72111 |
| Qy | 2150  | AGCAAGGCTGTTTTTGAAAATCATTACACTTTCCTAGTAAGCCCAAACCTCAGCATTCTG   | 2209  |
|    |       |  |       |
| Db | 72110 | AGCAAGGCTGTTTTTGAAAATCATTACACTTTCCTAGTAAGCCCAAACCTCAGCATTCTG   | 72051 |
| Qy | 2210  | CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC   | 2269  |
|    |       |  |       |
| Db | 72050 | CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC   | 71991 |
| Qy | 2270  | TGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG  | 2329  |
|    |       |  |       |
| Db | 71990 | TGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG  | 71931 |
| Qy | 2330  | ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA    | 2389  |
|    |       |  |       |
| Db | 71930 | ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA    | 71871 |
| Qy | 2390  | TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTTAA   | 2449  |
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| Db | 71870 | TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTTAA   | 71811 |
| Qy | 2450  | ATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT   | 2509  |
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| Db | 71810 | ATCTTCTTCTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT   | 71751 |
| Qy | 2510  | ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC   | 2569  |
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| Qy | 2570  | GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC   | 2629  |
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| Db | 71690 | GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC   | 71631 |
| Qy | 2630  | ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC   | 2689  |
|    |       |  |       |
| Db | 71630 | ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC   | 71571 |
| Qy | 2690  | ATATGTATAATGCTATAGTTAAATACTATTTTTCAAATCATACAGATTAGTACATTTA     | 2749  |
|    |       |  |       |
| Db | 71570 | ATATGTATAATGCTATAGTTAAATACTATTTTTCAAATCATACAGATTAGTACATTTA     | 71511 |

|    |       |  |       |
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| Qy | 2750  | ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTGTAAATAGCCAATAGAA    | 2809  |
|    |       |  |       |
| Db | 71510 | ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTGTAAATAGCCAATAGAA    | 71451 |
| Qy | 2810  | AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGT    | 2869  |
|    |       |  |       |
| Db | 71450 | AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGT    | 71391 |
| Qy | 2870  | AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCT    | 2929  |
|    |       |  |       |
| Db | 71390 | AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCT    | 71331 |
| Qy | 2930  | TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG   | 2989  |
|    |       |  |       |
| Db | 71330 | TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG   | 71271 |
| Qy | 2990  | GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTTCCCATTTCTAGCCTAACGTT  | 3049  |
|    |       |  |       |
| Db | 71270 | GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTTCCCATTTCTAGCCTAACGTT  | 71211 |
| Qy | 3050  | CGTCATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAACACAGTG       | 3109  |
|    |       |  |       |
| Db | 71210 | CGTCATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAACACAGTG       | 71151 |
| Qy | 3110  | CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA  | 3169  |
|    |       |  |       |
| Db | 71150 | CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA  | 71091 |
| Qy | 3170  | AATATGCCCAAATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA    | 3229  |
|    |       |  |       |
| Db | 71090 | AATATGCCCAAATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA    | 71031 |
| Qy | 3230  | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA    | 3289  |
|    |       |  |       |
| Db | 71030 | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA    | 70971 |
| Qy | 3290  | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT   | 3349  |
|    |       |  |       |
| Db | 70970 | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT   | 70911 |
| Qy | 3350  | ATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT | 3409  |
|    |       |  |       |
| Db | 70910 | ATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT | 70851 |
| Qy | 3410  | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA   | 3469  |
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| Db | 70850 | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA   | 70791 |
| Qy | 3470  | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACT    | 3529  |
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| Db | 70790 | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACT    | 70731 |
| Qy | 3530  | GAATTTTACATCCTGATACCTTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATC     | 3589  |
|    |       |  |       |
| Db | 70730 | GAATTTTACATCCTGATACCTTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATC     | 70671 |
| Qy | 3590  | TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA   | 3649  |

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|----|-------|--|--|-------|
| Db | 70670 |  | TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA | 70611 |
| Qy | 3650  |  | TTCAGTGGCTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA   | 3709  |
| Db | 70610 |  | TTCAGTGGCTTTTT-AAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA  | 70552 |
| Qy | 3710  |  | ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT | 3769  |
| Db | 70551 |  | ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT | 70492 |
| Qy | 3770  |  | TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA | 3829  |
| Db | 70491 |  | TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA | 70432 |
| Qy | 3830  |  | CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT | 3889  |
| Db | 70431 |  | CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT | 70372 |
| Qy | 3890  |  | CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC | 3949  |
| Db | 70371 |  | CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC | 70312 |
| Qy | 3950  |  | AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA  | 4009  |
| Db | 70311 |  | AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA  | 70252 |
| Qy | 4010  |  | TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA | 4069  |
| Db | 70251 |  | TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA | 70192 |
| Qy | 4070  |  | GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTA  | 4129  |
| Db | 70191 |  | GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTA  | 70132 |
| Qy | 4130  |  | CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAA | 4189  |
| Db | 70131 |  | CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAA | 70072 |
| Qy | 4190  |  | TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA | 4249  |
| Db | 70071 |  | TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA | 70012 |
| Qy | 4250  |  | GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG                        | 4286  |
| Db | 70011 |  | GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG                        | 69975 |

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 Job time : 1517.76 secs

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OM nucleic - nucleic search, using sw model

Run on: May 14, 2004, 00:25:48 ; Search time 266.574 Seconds  
(without alignments)  
8953.776 Million cell updates/sec

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Perfect score: 4301  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2             | 1691.8 | 39.3  | 1873   | 3  | US-08-910-864-13   | Sequence 13, Appl |
| 3             | 1466.8 | 34.1  | 1470   | 4  | US-09-016-434-1203 | Sequence 1203, Ap |
| 4             | 1070.4 | 24.9  | 1321   | 4  | US-09-175-658B-20  | Sequence 20, Appl |
| 5             | 395.8  | 9.2   | 4079   | 4  | US-09-016-434-1257 | Sequence 1257, Ap |
| 6             | 395.8  | 9.2   | 4105   | 4  | US-08-121-446-1    | Sequence 1, Appli |
| 7             | 132.2  | 3.1   | 1700   | 5  | PCT-US92-02091-1   | Sequence 1, Appli |
| 8             | 114.6  | 2.7   | 246240 | 2  | US-08-724-394A-20  | Sequence 20, Appl |
| 9             | 114.6  | 2.7   | 246240 | 2  | US-08-724-394A-21  | Sequence 21, Appl |
| 10            | 114.6  | 2.7   | 246240 | 2  | US-08-724-394A-22  | Sequence 22, Appl |
| 11            | 108.8  | 2.5   | 1584   | 5  | PCT-US92-02091-5   | Sequence 5, Appli |

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| c | 12 | 107.2 | 2.5 | 801    | 4 | US-09-175-658B-25  | Sequence 25, Appl |
|   | 13 | 106.6 | 2.5 | 1205   | 3 | US-09-120-772-1    | Sequence 1, Appli |
|   | 14 | 106.6 | 2.5 | 1413   | 4 | US-09-016-434-1275 | Sequence 1275, Ap |
|   | 15 | 106   | 2.5 | 1726   | 4 | US-09-016-434-1215 | Sequence 1215, Ap |
|   | 16 | 106   | 2.5 | 1726   | 5 | PCT-US92-02091-3   | Sequence 3, Appli |
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|   | 21 | 89.6  | 2.1 | 259    | 4 | US-09-016-434-921  | Sequence 921, App |
|   | 22 | 88    | 2.0 | 1842   | 4 | US-09-170-496D-91  | Sequence 91, Appl |
|   | 23 | 88    | 2.0 | 1842   | 4 | US-09-170-496D-211 | Sequence 211, App |
|   | 24 | 88    | 2.0 | 4953   | 4 | US-09-620-312D-240 | Sequence 240, App |
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|   | 27 | 84.8  | 2.0 | 4156   | 4 | US-09-520-210-1    | Sequence 1, Appli |
|   | 28 | 84.8  | 2.0 | 4156   | 5 | PCT-US94-11843-1   | Sequence 1, Appli |
|   | 29 | 80.6  | 1.9 | 1443   | 3 | US-08-959-381A-3   | Sequence 3, Appli |
|   | 30 | 80.6  | 1.9 | 1446   | 4 | US-09-170-496D-81  | Sequence 81, Appl |
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|   | 32 | 80.6  | 1.9 | 1626   | 3 | US-08-959-381A-4   | Sequence 4, Appli |
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| c | 34 | 63.4  | 1.5 | 20674  | 4 | US-09-641-638-651  | Sequence 651, App |
|   | 35 | 63.2  | 1.5 | 595    | 1 | US-08-784-289-1    | Sequence 1, Appli |
|   | 36 | 62.8  | 1.5 | 1652   | 4 | US-09-721-870-17   | Sequence 17, Appl |
|   | 37 | 61.8  | 1.4 | 1605   | 4 | US-09-676-970-1    | Sequence 1, Appli |
|   | 38 | 61.8  | 1.4 | 1605   | 4 | US-09-676-972B-1   | Sequence 1, Appli |
|   | 39 | 61.8  | 1.4 | 1605   | 4 | US-09-016-434-1231 | Sequence 1231, Ap |
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|   | 44 | 60.8  | 1.4 | 511    | 4 | US-09-175-658B-22  | Sequence 22, Appl |
| c | 45 | 60.6  | 1.4 | 1864   | 4 | US-09-468-265-4    | Sequence 4, Appli |

#### ALIGNMENTS

#### RESULT 1

US-08-121-446-3

; Sequence 3, Application US/08121446

; Patent No. 6313276

; GENERAL INFORMATION:

; APPLICANT: IMURA, HIROO

; APPLICANT: NAKAO, KAZUWA

; APPLICANT: NAKANISHI, SHIGETADA

; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,446
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,684
; FILING DATE: 10-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 29900-20324.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 238..1566
US-08-121-446-3

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Query Match          100.0%; Score 4301; DB 4; Length 4301;
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Matches 4301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Qy | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420  |
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| Db | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420  |
| Qy | 421  | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG  | 480  |
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| Qy | 481  | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540  |
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| Qy | 541  | TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGA          | 600  |
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| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
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| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
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| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
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| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT    | 1380 |
|    |      |  |      |
| Db | 1321 | AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT    | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA     | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA     | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
|    |      |  |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCAGTAATAAATACAGCTCA    | 1560 |
|    |      |  |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCAGTAATAAATACAGCTCA    | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTCACTTTCTTTATATTGGACCGAAGTCATTAA   | 1620 |
|    |      |  |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTCACTTTCTTTATATTGGACCGAAGTCATTAA   | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAAGCTATGTATTTGCACAGCACACTAT  | 1680 |
|    |      |  |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAAGCTATGTATTTGCACAGCACACTAT  | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
|    |      |  |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
|    |      |  |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
|    |      |  |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA   | 1920 |
|    |      |  |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA   | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG  | 1980 |
|    |      |  |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG  | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAAATTTAAAAATCCTTTAAAAACAACCTTTCAATTAATAT | 2040 |
|    |      |  |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAAAATTTAAAAATCCTTTAAAAACAACCTTTCAATTAATAT | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |

|    |      |   |      |
|----|------|---|------|
| Db | 2041 | <br>TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT      | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCCAAACCTCAGCATTCTGCAATATGTAAC     | 2220 |
| Db | 2161 | <br>TTTTGAAAATCATTACACTTTCACTAGAAGCCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA      | 2280 |
| Db | 2221 | <br>CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA       | 2340 |
| Db | 2281 | <br>TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA       | 2400 |
| Db | 2341 | <br>CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT      | 2460 |
| Db | 2401 | <br>CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT  | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA      | 2520 |
| Db | 2461 | <br>TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT      | 2580 |
| Db | 2521 | <br>CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG       | 2640 |
| Db | 2581 | <br>GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT      | 2700 |
| Db | 2641 | <br>GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT  | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG       | 2760 |
| Db | 2701 | <br>GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG      | 2820 |
| Db | 2761 | <br>TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCCAAAACCTGCTTTTGAGACCGTAAGAACCTCTT     | 2880 |
| Db | 2821 | <br>ACATGGTGCTTTTCTTTCATCTAGAGGCCAAAACCTGCTTTTGAGACCGTAAGAACCTCTT | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT      | 2940 |
|    |      |   |      |

|    |      |   |      |
|----|------|---|------|
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
|    |      |   |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
|    |      |   |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCTTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |
|    |      |   |      |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCTTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA | 3180 |
|    |      |   |      |
| Db | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA | 3180 |
| Qy | 3181 | ATTTTACTTTGTTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
|    |      |   |      |
| Db | 3181 | ATTTTACTTTGTTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA    | 3300 |
|    |      |   |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA    | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
|    |      |   |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
| Qy | 3361 | ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |   |      |
| Db | 3361 | ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
|    |      |   |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTACA   | 3540 |
|    |      |   |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTACA   | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
|    |      |   |      |
| Db | 3541 | TCCTGATACCCTTTCCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
|    |      |   |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
|    |      |   |      |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT  | 3780 |
|    |      |   |      |
| Db | 3721 | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT  | 3780 |

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 Qy 3841 CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3841 CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTTC 4140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTTC 4140  
 Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAAAAA 4301  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAAAAA 4301

RESULT 2

US-08-910-864-13

; Sequence 13, Application US/08910864

; Patent No. 6280931

; GENERAL INFORMATION:

; APPLICANT: SAKAMOTO, AIJI

; APPLICANT: HANAOKA, FUMIO

; TITLE OF INVENTION: METHOD FOR SPECIFICALLY AMPLIFYING A cDNA OF AN  
 EXTREMELY

; TITLE OF INVENTION: SMALL QUANTITY

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FISH & RICHARDSON P.C.

; STREET: 4225 EXECUTIVE SQUARE, SUITE 1400

; CITY: LA JOLLA

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,864
; FILING DATE: 13-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 216506/1996
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILE, LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07898/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1873 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 231..1556
US-08-910-864-13

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Query Match          39.3%; Score 1691.8; DB 3; Length 1873;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1696; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237
      || || |||||
Db      171 TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 230

Qy      238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297
      |||||
Db      231 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 290

Qy      298 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 357
      |||||
Db      291 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 350

Qy      358 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 417
      |||||
Db      351 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 410

Qy      418 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 477
      |||||
Db      411 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 470

Qy      478 CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 537
      |||||
Db      471 CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 530

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|    |      |  |      |
|----|------|--|------|
| Qy | 538  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC | 597  |
|    |      |  |      |
| Db | 531  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC | 590  |
| Qy | 598  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 657  |
|    |      |  |      |
| Db | 591  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 650  |
| Qy | 658  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 717  |
|    |      |  |      |
| Db | 651  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 710  |
| Qy | 718  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA   | 777  |
|    |      |  |      |
| Db | 711  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA   | 770  |
| Qy | 778  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 837  |
|    |      |  |      |
| Db | 771  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 830  |
| Qy | 838  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA   | 897  |
|    |      |  |      |
| Db | 831  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA   | 890  |
| Qy | 898  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 957  |
|    |      |  |      |
| Db | 891  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 950  |
| Qy | 958  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1017 |
|    |      |  |      |
| Db | 951  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1010 |
| Qy | 1018 | CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTC  | 1077 |
|    |      |  |      |
| Db | 1011 | CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTATTTCAGTTTC  | 1070 |
| Qy | 1078 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG  | 1137 |
|    |      |  |      |
| Db | 1071 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG  | 1130 |
| Qy | 1138 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA   | 1197 |
|    |      |  |      |
| Db | 1131 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA   | 1190 |
| Qy | 1198 | GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC   | 1257 |
|    |      |  |      |
| Db | 1191 | GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC   | 1250 |
| Qy | 1258 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT   | 1317 |
|    |      |  |      |
| Db | 1251 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT   | 1310 |
| Qy | 1318 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC   | 1377 |
|    |      |  |      |
| Db | 1311 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC   | 1370 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1378 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTGCTTTAAGTCATGC | 1437 |
|    |      |   |      |
| Db | 1371 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTGCTTTAAGTCATGC | 1430 |
| Qy | 1438 | TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC  | 1497 |
|    |      |   |      |
| Db | 1431 | TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC  | 1490 |
| Qy | 1498 | TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC  | 1557 |
|    |      |   |      |
| Db | 1491 | TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC  | 1550 |
| Qy | 1558 | TCATCTTGAAAGAAGAACTATTCAGTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT | 1617 |
|    |      |   |      |
| Db | 1551 | TCATCTTGAAAGAAGAACTATTCAGTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT | 1610 |
| Qy | 1618 | TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC  | 1677 |
|    |      |   |      |
| Db | 1611 | TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC  | 1670 |
| Qy | 1678 | TATTTAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGC    | 1737 |
|    |      |   |      |
| Db | 1671 | TATTTAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGC    | 1730 |
| Qy | 1738 | TGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT   | 1797 |
|    |      |   |      |
| Db | 1731 | TGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT   | 1790 |
| Qy | 1798 | AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC  | 1857 |
|    |      |   |      |
| Db | 1791 | AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC  | 1850 |
| Qy | 1858 | ACTTAGGCTTAAAAATGAGCTCA                                       | 1880 |
|    |      |   |      |
| Db | 1851 | ACTTAGGCTTAAAAATGAGCTCA                                       | 1873 |

# RESULT 3

US-09-016-434-1203

; Sequence 1203, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/016,434
;   FILING DATE:  HERewith
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Zeller, Karen J.
;   REGISTRATION NUMBER:  37,071
;   REFERENCE/DOCKET NUMBER:  PA-0002 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (650) 855-0555
;   TELEFAX:  (650) 845-4166
;   INFORMATION FOR SEQ ID NO:  1203:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1470 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   IMMEDIATE SOURCE:
;   LIBRARY:  GENBANK
;   CLONE:  g182275
US-09-016-434-1203

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Query Match          34.1%;  Score 1466.8;  DB 4;  Length 1470;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 1468;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

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Qy      192  GAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC 251
          |||
Db      1    GAAACTGCGGACGGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC 60

Qy      252  AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGGATCTG 311
          |||
Db      61  AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGGATCTG 120

Qy      312  GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGAT 371
          |||
Db      121  GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGAT 180

Qy      372  AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC 431
          |||
Db      181  AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC 240

Qy      432  GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT 491
          |||
Db      241  GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT 300

Qy      492  CTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC 551
          |||
Db      301  CTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC 360

Qy      552  GGTTGTGTCTGCCTTGTGTTCTGCTGGGGATCATCGGGAAGTCCACACTTCTGAGAAT 611

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|    |      |  |  |      |
|----|------|--|--|------|
| Db | 361  |  | GGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAAT | 420  |
| Qy | 612  |  | TATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCT   | 671  |
| Db | 421  |  | TATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCT   | 480  |
| Qy | 672  |  | GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA   | 731  |
| Db | 481  |  | GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA   | 540  |
| Qy | 732  |  | GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGT   | 791  |
| Db | 541  |  | GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGT   | 600  |
| Qy | 792  |  | GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC   | 851  |
| Db | 601  |  | GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC   | 660  |
| Qy | 852  |  | TTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGAT   | 911  |
| Db | 661  |  | TTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGAT   | 720  |
| Qy | 912  |  | TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGAT   | 971  |
| Db | 721  |  | TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGAT   | 780  |
| Qy | 972  |  | GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT   | 1031 |
| Db | 781  |  | GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT   | 840  |
| Qy | 1032 |  | CATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTTGCC  | 1091 |
| Db | 841  |  | CATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTTGCC  | 900  |
| Qy | 1092 |  | ATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAG  | 1151 |
| Db | 901  |  | ATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAG  | 960  |
| Qy | 1152 |  | TGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGT   | 1211 |
| Db | 961  |  | TGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGT   | 1020 |
| Qy | 1212 |  | CTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCT   | 1271 |
| Db | 1021 |  | CTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCT   | 1080 |
| Qy | 1272 |  | GAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTT   | 1331 |
| Db | 1081 |  | GAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTT   | 1140 |
| Qy | 1332 |  | GGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGC   | 1391 |
| Db | 1141 |  | GGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGC   | 1200 |
| Qy | 1392 |  | TCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGCTGGTG  | 1451 |
|    |      |  |  |      |

Db 1201 TCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTATGCTGCTGGTG 1260

Qy 1452 CCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGC 1511  
 |||

Db 1261 CCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGC 1320

Qy 1512 TAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAA 1571  
 |||

Db 1321 TAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAA 1380

Qy 1572 GAACTATTCACTGTATTTTCTTTATATTGGACCGAAGTCATTAAACAAAATGAA 1631  
 |||

Db 1381 GAACTATTCACTGTATTTTCTTTATATTGGACCGAAGTCATTAAACAAAATGAA 1440

Qy 1632 ACATTTGCCAAAACAAAACAAAAAACTATG 1661  
 |||

Db 1441 ACATTTGCCAAAACAAAACAAAAAACTATG 1470

#### RESULT 4

US-09-175-658B-20

; Sequence 20, Application US/09175658B

; Patent No. 6372900

; GENERAL INFORMATION:

; APPLICANT: METALLINOS, DANIKA

; APPLICANT: RINE, JASPER

; APPLICANT: BOWLING, ANN

; TITLE OF INVENTION: HORSE ENDOTHELIN-B RECEPTOR GENE AND GENE PRODUCTS

; FILE REFERENCE: GOBR-110

; CURRENT APPLICATION NUMBER: US/09/175,658B

; CURRENT FILING DATE: 1998-10-20

; PRIOR APPLICATION NUMBER: 60/062,562

; PRIOR FILING DATE: 1997-10-21

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 1321

; TYPE: DNA

; ORGANISM: Horse

US-09-175-658B-20

Query Match 24.9%; Score 1070.4; DB 4; Length 1321;  
 Best Local Similarity 88.7%; Pred. No. 1.5e-256;  
 Matches 1171; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

Qy 227 CAGGTAGCAGCATGCAGCCGCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTC 286  
 |||

Db 1 CAGGTAGCAGCATGCAGCCTCTGCCAACCCTGTGTGGACGCGTTCTGGTGGCGCTGATCC 60

Qy 287 TTGCCTGCGGCCTGTGCGGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCA 346  
 |||

Db 61 TTGCCTGCGGCGTGGCAGGGGTCCAGGGAGAAGAGAGGAGATTCCCGCCGGCCAGGGCCA 120

Qy 347 CTCCG---CTTTTGCAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCA 403  
 |||

Db 121 CTCCGCCACTTCTGGGGTCTGAAGAGATAATGACGCCCCGACTAAGACCTCCTGGCCGA 180

|    |      |  |      |
|----|------|--|------|
| QY | 404  | AGGGTTCCAACGCCAGTCTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACA  | 463  |
|    |      |  |      |
| Db | 181  | CGGGGTCCAACGCCAGCGTGCCGCGGTTCATCAGCACCTCCGCAAATGCCTAAAGCAGGGA  | 240  |
| QY | 464  | GGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGA   | 523  |
|    |      |  |      |
| Db | 241  | GGACGGCGGGAGCCCAGCGACGCACCCTCCCTCCTCCCCCGTGCGAAAGAACCATCGAGA   | 300  |
| QY | 524  | TCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTGCTTGTGTTTCGTGCTGGGGA    | 583  |
|    |      |  |      |
| Db | 301  | TCAAGGAGACTTTCAAGTACATCAACACAGTAGTGTCTGCTTAGTGTTTCGTGCTGGGCA   | 360  |
| QY | 584  | TCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTC  | 643  |
|    |      |  |      |
| Db | 361  | TCATCGGAAACTCCACACTGCTGAGAATCATTTACAAGAACAAGTGCATGCGGAACGGCC   | 420  |
| QY | 644  | CCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCC   | 703  |
|    |      |  |      |
| Db | 421  | CTAATATCTTGATCGCCAGCCTGGCTCTCCGAGACCTGCTGCAAATCATCATTGACGTCC   | 480  |
| QY | 704  | CTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGC   | 763  |
|    |      |  |      |
| Db | 481  | CCATCAATGTCTACAAGCTGCTGGCTGAGGACTGGCCCTTTGGAGTCGAGATGTGTAAGC   | 540  |
| QY | 764  | TGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGA  | 823  |
|    |      |  |      |
| Db | 541  | TGGTGCCTTTTCATACAGAAGGCCTCCGTGGGCATCACTGTGCTGAGTCTGTGTGCTCTAA  | 600  |
| QY | 824  | GTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAA   | 883  |
|    |      |  |      |
| Db | 601  | GTATTGACAGATATCGAGCTGTTGCTTCCCTTGGAGCGAATTAAAGGAATTCGGGTTCAA   | 660  |
| QY | 884  | AATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTG   | 943  |
|    |      |  |      |
| Db | 661  | AATGGACAGCAGTAGAAATTGTTTTAATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTG   | 720  |
| QY | 944  | AAGCCATAGTTTTTGATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCT   | 1003 |
|    |      |  |      |
| Db | 721  | AAGCCGTGGGTTTTGATATGATTACCGCTGACTACAAAGGAAGTTATCTGCGAATCTGCC   | 780  |
| QY | 1004 | TGCTTCATCCCGTTTCAGAAGACAGCTTTCATGCAGTTTACAAAGACAGCAAAGATTGGT   | 1063 |
|    |      |  |      |
| Db | 781  | TGCTTCATCCCACTCAGAAAACAGCCTTCATGCAGTTTACAAAGATGCTAAGGACTGGT    | 840  |
| QY | 1064 | GGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAA | 1123 |
|    |      |  |      |
| Db | 841  | GGCTATTTAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACCTTGA  | 900  |
| QY | 1124 | TGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAA   | 1183 |
|    |      |  |      |
| Db | 901  | TGACCTGTGAAATGTTGAGAAAGAAGAGTGGCATGCAAATTGCTTTAAATGATCACTTAA   | 960  |
| QY | 1184 | AGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCT   | 1243 |
|    |      |  |      |
| Db | 961  | AGCAGAGAAGGGAAGTGGCGAAAACAGTATTCTGCCTGGTCCTTGTCTTTGCCCTGTGCT   | 1020 |
| QY | 1244 | GGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCA   | 1303 |

|    |      |  |  |      |
|----|------|--|--|------|
| Db | 1021 |  | GGCTTCCTCTTCACCTCAGCAGGATTTTGAAACACACTCTTTATGATCAGAATGATCCCC | 1080 |
| Qy | 1304 |  | ATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTT | 1363 |
| Db | 1081 |  | ATAGATGTGAACTTTTGAGCTTTTGTGTTGATTTGGACTACATTGGCATCAACATGGCCT | 1140 |
| Qy | 1364 |  | CACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC  | 1423 |
| Db | 1141 |  | CCCTGAATTCCTGCATTAATCCAATAGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC  | 1200 |
| Qy | 1424 |  | GCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGG | 1483 |
| Db | 1201 |  | GCTTTAAGTCGTGCTTATGCTGCTGGTGCCAATCATTTGAAGAAAAACAGTCCTTGAAG  | 1260 |
| Qy | 1484 |  | AAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCA | 1543 |
| Db | 1261 |  | ACAAGCAGTCATGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCA | 1320 |

RESULT 5

US-09-016-434-1257

; Sequence 1257, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

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; INFORMATION FOR SEQ ID NO: 1257:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4079 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: GENBANK
;   CLONE: g219649
US-09-016-434-1257
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Query Match          9.2%; Score 395.8; DB 4; Length 4079;
Best Local Similarity 65.7%; Pred. No. 2.5e-88;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;
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Qy      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTGC 564
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Db      685 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 744

Qy      565 CTTGTGTTCGTGCTGGGGATCATCGGGAACCCACACTTCTGAGAATTATCTACAAGAAC 624
      | | || | | |||| | | | | | | | | | | | | | |
Db      745 ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 804

Qy      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684
      || || || | | | | |||| | | | | | | | | | |
Db      805 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGGAGACCTTATC 864

Qy      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740
      | | |||| | | | | | | | | | | | | | | | |
Db      865 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCCTTTT 924

Qy      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789
      |||| | | | | | | | | | | | | | | | | | |
Db      925 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTGCAGAAGTCCTCG 984

Qy      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849
      |||| |||| | | | | | | | | | | | | | | | |
Db      985 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1044

Qy      850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAATGGACAGCAGTAGAAATTGTTTTG 909
      || |||| | | | | | | | | | | | | | | | |
Db      1045 TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCTTTGGTAAGTCCATTGAAATTGTCTCC 1104

Qy      910 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969
      || || | | | | | | | | | | | | | | | | |
Db      1105 ATCTGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTATGGTACCC 1164

Qy      970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT 1029
      | | || | | | | | | | | | | | | | | | |
Db      1165 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1218

Qy      1030 TTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTG 1089
      |||| | | | | | | | | | | | | | | | | |
Db      1219 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1278

Qy      1090 CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG 1146
      || || | | | | | | | | | | | | | | | | |
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Db 1279 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1338

Qy 1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206  
 || | ||| || |||| | | ||| || || ||||| | || ||||| |||

Db 1339 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1398

Qy 1207 ACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCCTTCACCTCAGCAGG 1266  
 || || || |||| |||| | | ||||| || ||||| | || ||||| | ||| |

Db 1399 ACAGTTTCTGCTTGTTGTAATTTTGTCTTTGCTGGTTCCCTCTTCACTTAAGCCGT 1458

Qy 1267 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTT 1326  
 || ||||| ||| | ||||| | | || || ||||| | | || ||

Db 1459 ATATTGAAGAAAAGTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1518

Qy 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386  
 | || | |||| || || |||| || |||| | ||||| || || |||||

Db 1519 TTAAGTCTCATGGATTACATCGGTATTAAGTGGCAACCATGAATTCATGTATAAACCCC 1578

Qy 1387 ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGC 1446  
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Db 1579 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATGTTTCCAGTCATGCCTCTGCTGC 1638

Qy 1447 TGGTG 1451  
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Db 1639 TGCTG 1643

RESULT 6

US-08-121-446-1

; Sequence 1, Application US/08121446  
 ; Patent No. 6313276  
 ; GENERAL INFORMATION:  
 ; APPLICANT: IMURA, HIROO  
 ; APPLICANT: NAKAO, KAZUWA  
 ; APPLICANT: NAKANISHI, SHIGETADA  
 ; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/121,446  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/911,684  
 ; FILING DATE: 10-JUL-1992  
 ; ATTORNEY/AGENT INFORMATION:

```

; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 29900-20324.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4105 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 485..1768
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 545
US-08-121-446-1

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Query Match          9.2%; Score 395.8; DB 4; Length 4105;
Best Local Similarity 65.7%; Pred. No. 2.5e-88;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

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Qy      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCTGC 564
      |||| |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      689 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748

Qy      565 CTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 624
      |  |  ||| |  |||| |  |  |||| |  |  |||| |  |  |||| |  |  |||| |  |
Db      749 ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808

Qy      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684
      || || ||| |  || || |||| |  |||| |||| |  || || |||| ||| |  |
Db      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC 868

Qy      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740
      |  |  |||| ||| |  |||| |||| ||| |  |||| |||| |  |  |||| |
Db      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCCTTTT 928

Qy      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789
      |||| |  |  |  |||| |  |  || ||  |  |||| |  |||
Db      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTGCAGAAGTCCTCG 988

Qy      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849
      |||| |  |||| |  || || |  || || |||| |  |||| ||| ||| |||| |
Db      989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1048

Qy      850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909
      || |||| |  |  |  |||| |||| |||| |  || || |  |||| ||| |
Db      1049 TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCTTTGGTAAGTCCATTGAAATTGTCTCC 1108

Qy      910 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969
      || ||| |  |  || |  |  |||| |  |||| ||| || || || |  |  |
Db      1109 ATCTGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATGGTACCC 1168

```

Qy 970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT 1029  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222  
 Qy 1030 TTCATGCAGTTTACAAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTTG 1089  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1282  
 Qy 1090 CCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAAG 1146  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1283 CCCTTGGTGTGCACTGCGATCTTCTACACCTCATGACTTGTGAGATGTTGAACAGAAGG 1342  
 Qy 1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402  
 Qy 1207 ACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTCAGCAGG 1266  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1403 ACAGTTTCTGCTTGGTTGTAATTTTGTCTTTGCTGGTTCCCTCTTCACTTAAGCCGT 1462  
 Qy 1267 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTT 1326  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1463 ATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522  
 Qy 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1523 TTAAGTCTCATGGATTACATCGGTATTAAGTGGCAACCATGAATTCATGTATAAACCCC 1582  
 Qy 1387 ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC 1446  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642  
 Qy 1447 TGGTG 1451  
 | | | |  
 Db 1643 TGCTG 1647

# RESULT 7

PCT-US92-02091-1

; Sequence 1, Application PC/TUS9202091

## ; GENERAL INFORMATION:

; APPLICANT: Battey Jr., James F.

; APPLICANT: Corjay, Martha H.

; APPLICANT: Feldman, Richard I.

; APPLICANT: Harkins, Richard N.

; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwin P. Ching

; STREET: 1501 Harbor Bay Parkway

; CITY: Alameda

; STATE: CA

; COUNTRY: USA

; ZIP: 94501

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible



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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US92/02091
;   FILING DATE:  19920313
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/426,150
;   FILING DATE:  24-OCT-1989
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/533,659
;   FILING DATE:  05-JUN-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Ching, Edwin P.
;   REGISTRATION NUMBER:  34090
;   REFERENCE/DOCKET NUMBER:  A-0092C
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-266-7476
;   TELEFAX:  415-266-7400
;   INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1700 base pairs
;   TYPE:  NUCLEIC ACID
;   STRANDEDNESS:  double
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA to mRNA
;   HYPOTHETICAL:  NO
;   ORIGINAL SOURCE:
;   ORGANISM:  Mus musculus
;   CELL LINE:  Swiss 3T3
;   IMMEDIATE SOURCE:
;   LIBRARY:  Lambda GT10
;   FEATURE:
;   NAME/KEY:  CDS
;   LOCATION:  378..1532
PCT-US92-02091-1

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Query Match          3.1%;  Score 132.2;  DB 5;  Length 1700;
Best Local Similarity  56.9%;  Pred. No. 6.4e-23;
Matches 242;  Conservative  0;  Mismatches 183;  Indels  0;  Gaps  0;

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Qy      535 TTCAAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAC 594
        ||||  ||  |||  |  |  |  |  |  |  |  |||  |  ||||  |  ||  |  ||  |||
Db      495 TTCATCTATGTCATCCCTGCAGTTTATGGGCTTATCATCGTGATAGGTCTTATTGGCAAC 554

Qy      595 TCCACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTG 654
        |||  ||  |  |  ||  |||  ||  |  ||||  |||||  ||||  ||  ||  |  ||
Db      555 ATCACGCTCATCAAGATCTTCTGCACGGTCAAGTCCATGCGAAACGTGCCAAACCTGTTC 614

Qy      655 ATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTC 714
        |||  |  |||  ||||  |||||  |||||  |||||  ||  ||  |  ||||  |  |||  |
Db      615 ATCTCTAGCCTGGCTTTGGGAGACCTGCTGCTGCTGGTGACATGCGCCCCTGTGGATGCC 674

Qy      715 TACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTC 774
        ||||  ||||  ||  |||  ||||  ||||  ||  ||  |||  |  ||  ||
Db      675 AGCAAGTACCTGGCTGACAGGTGGCTATTTGGCAGAATTGGCTGCAAACCTGATCCCCTTT 734

```

Qy 775 ATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGA 834  
 ||||| | || ||||| | |||| | | || || |||||  
 Db 735 ATACAACTTACTTCAGTGGGGGTGTCTGTCTTCACACTTACGGCACTGTCAGCTGACAGG 794  
 Qy 835 TATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCA 894  
 || ||| ||| | || | | | | | | ||  
 Db 795 TACAAAGCCATTGTACGGCCAATGGATATCCAGGCATCCCATGCCCTGATGAAGATCTGT 854  
 Qy 895 GTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGT 954  
 | || || ||||| ||| | ||||| || | |||| |||| || || |  
 Db 855 CTCAAAGCTGCTTTGATCTGGATTGTCTCTATGTTGTTGGCCATCCCAGAGGCTGTGTTT 914  
 Qy 955 TTTGA 959  
 | |||  
 Db 915 TCTGA 919

RESULT 8

US-08-724-394A-20

; Sequence 20, Application US/08724394A

; Patent No. 5872237

; GENERAL INFORMATION:

; APPLICANT: Feder, John N.

; APPLICANT: Kronmal, Gregory S.

; APPLICANT: Lauer, Peter M.

; APPLICANT: Ruddy, David A.

; APPLICANT: Thomas, Winston

; APPLICANT: Tsuchihashi, Zenta

; APPLICANT: Wolff, Roger K.

; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1

; TITLE OF INVENTION: Sequences and Antibodies Thereto

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/724,394A

; FILING DATE: 01-OCT-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitts, Renee A.

; REGISTRATION NUMBER: 35,136

; REFERENCE/DOCKET NUMBER: 017957-000100

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-576-0200

; TELEFAX: 415-576-0300

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

```
;   LENGTH: 246240 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: not relevant
;   TOPOLOGY: not relevant
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: misc_feature
;     LOCATION: 1..246240
;     OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
```

```
Query Match          2.7%;   Score 114.6;   DB 2;   Length 246240;
Best Local Similarity 82.0%;   Pred. No. 2.5e-17;
Matches 132;   Conservative 0;   Mismatches 29;   Indels 0;   Gaps 0;
```

```
Qy          5 CATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCCAGGT 64
      ||| || |||| |||| |||| |||| || || |||| ||||| ||||| |||
Db   180691 CATCCCTACGGGGAAGTCCAGCCAGTTTGAGCGACACAGATCTGGAGAGCGCTCCCAGGT
180750
```

```
Qy          65 AGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGGAGGA 124
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db   180751 AGGCAATTGCCCCGGTGGAAACGCCTCACCAGAGCAGCACGTGGCAGGCCCTCGTGGAGGA
180810
```

```
Qy          125 TCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGG 165
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db   180811 TCAACGCAGTGGCTGAACACCGGGAAGGAACTGGCACTTTG 180851
```

# RESULT 9

US-08-724-394A-21

```
; Sequence 21, Application US/08724394A
; Patent No. 5872237
```

## GENERAL INFORMATION:

```
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21

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Query Match          2.7%; Score 114.6; DB 2; Length 246240;
Best Local Similarity 82.0%; Pred. No. 2.5e-17;
Matches 132; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

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```

Qy          5 CATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCCAGGT 64
             ||| ||   ||| ||| ||| ||| ||| ||   ||| ||| ||| ||| |||
Db    180691 CATCCCTACGGGGAAGTCCAGCCAGTTTGAGCGACACAGATCTGGAGAGCGCTCCCAGGT
180750

Qy          65 AGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGGAGGA 124
             ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    180751 AGGCAATTGCCCCGGTGGAAACGCCTCACCAGAGCAGCACGTGGCAGGCCCTCGTGGAGGA
180810

Qy          125 TCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGG 165
             ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    180811 TCAACGCAGTGGCTGAACACCGGGAAGGAACTGGCACTTTG 180851

```

RESULT 10

US-08-724-394A-22

; Sequence 22, Application US/08724394A

; Patent No. 5872237

; GENERAL INFORMATION:

; APPLICANT: Feder, John N.

; APPLICANT: Kronmal, Gregory S.

; APPLICANT: Lauer, Peter M.

; APPLICANT: Ruddy, David A.

; APPLICANT: Thomas, Winston

; APPLICANT: Tsuchihashi, Zenta

; APPLICANT: Wolff, Roger K.

; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1

; TITLE OF INVENTION: Sequences and Antibodies Thereto

```

; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22

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Query Match          2.7%; Score 114.6; DB 2; Length 246240;
Best Local Similarity 82.0%; Pred. No. 2.5e-17;
Matches 132; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

```

```

Qy          5 CATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCCAGGT 64
             ||| ||  |||| ||||  ||||  |||| ||  ||||  |||||  |||||
Db    180691 CATCCCTACGGGGAAGTCCAGCCAGTTTGTAGCGACACAGATCTGGAGAGCGCTCCCAGGT
180750

Qy          65 AGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGGAGGA 124
             |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db    180751 AGGCAATTGCCCCGGTGGAAACGCCTCACCAGAGCAGCACGTGGCAGGCCCTCGTGGAGGA
180810

Qy          125 TCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGG 165
             |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db    180811 TCAACGCAGTGGCTGAACACCGGGAAGGAACTGGCACTTTG 180851

```

RESULT 11

PCT-US92-02091-5  
; Sequence 5, Application PC/TUS9202091  
; GENERAL INFORMATION:  
; APPLICANT: Battey Jr., James F.  
; APPLICANT: Corjay, Martha H.  
; APPLICANT: Feldman, Richard I.  
; APPLICANT: Harkins, Richard N.  
; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Edwin P. Ching  
; STREET: 1501 Harbor Bay Parkway  
; CITY: Alameda  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94501  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/02091  
; FILING DATE: 19920313  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/426,150  
; FILING DATE: 24-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/533,659  
; FILING DATE: 05-JUN-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34090  
; REFERENCE/DOCKET NUMBER: A-0092C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-266-7476  
; TELEFAX: 415-266-7400  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1584 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Rattus rattus  
; TISSUE TYPE: Esophagus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 132..1304  
PCT-US92-02091-5

Query Match 2.5%; Score 108.8; DB 5; Length 1584;  
Best Local Similarity 54.8%; Pred. No. 4.1e-17;  
Matches 215; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

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|----|-----|--|-----|
| Qy | 572 | TCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAACAAGTGCA  | 631 |
|    |     |  |     |
| Db | 292 | TCTCGGTGGGCTTGCTGGGGCAACATCATGCTGGTGAAGATATTCCTCACCAACAGCACCA  | 351 |
| Qy | 632 | TGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCG   | 691 |
|    |     |  |     |
| Db | 352 | TGCGGAGTGTCCCCAACATCTTCATCTCTAACCTGGCTGCGGGAGACCTGCTGCTGCTGC   | 411 |
| Qy | 692 | TCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTG   | 751 |
|    |     |  |     |
| Db | 412 | TGACCTGCGTCCCAGTGGATGCCTCCCGATACTTCTTTGATGAATGGGTGTTCTCGGCAAGC | 471 |
| Qy | 752 | AGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTC   | 811 |
|    |     |  |     |
| Db | 472 | TGGGCTGCAAACCTCATCCCAGCCATCCAGCTCACCTCGGTGGGGGTTTCCGTGTTCACTC  | 531 |
| Qy | 812 | TATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGAGTAGAATTAAAGGAA    | 871 |
|    |     |  |     |
| Db | 532 | TCACGGCCCTCAGCGTGACAGGTACAGAGCTATCGTGAACCCCATGGACATGCAGACGT    | 591 |
| Qy | 872 | TTGGGGTTCCAAAATGGACAGCAGTAGAAATGTTTTGATTTGGGTGGTCTCTGTGGTTT    | 931 |
|    |     |  |     |
| Db | 592 | CTGGTGTGGTGTCTGTGGACCAGTTTGAAGGCCGTGGGCATCTGGGTGGTCTCTGTGCTGT  | 651 |
| Qy | 932 | TGGCTGTCCCTGAAGCCATAGGTTTTGATATA                               | 963 |
|    |     |  |     |
| Db | 652 | TGGCTGTCCCTGAGGCTGTGTTTTTCGGAAGTA                              | 683 |

## RESULT 12

US-09-175-658B-25/c

; Sequence 25, Application US/09175658B

; Patent No. 6372900

## ; GENERAL INFORMATION:

; APPLICANT: METALLINOS, DANIKA

; APPLICANT: RINE, JASPER

; APPLICANT: BOWLING, ANN

10 TITLE OF INVENTION: HORSE ENDOTHELIN-B RECEPTOR GENE AND GENE PRODUCTS

; FILE REFERENCE: GOBR-110

; CURRENT APPLICATION NUMBER: US/09/175,658B

: CURRENT FILING DATE: 1998-10-20

: PRIOR APPLICATION NUMBER: 60/062,562

; PRIOR FILING DATE: 1997-10-21

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; NUMBER OF SEQ ID NOS: 25
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: SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 25

; LENGTH: 801

; TYPE: DNA

ORGANISM: Horse

; FEATURE:

; OTHER INFORMATION: Uncertain of the nucleotide sequence at positions

OTHER INFORMATION: 30, 54, 286, 436, 445, 542, 614, 617, 624, 641,

OTHER INFORMATION: 731, 746, 753, 770, 775 and 793.

US-09-175-658B-25

Query Match

2.5%; Score 107.2; DB 4; Length 801;

Best Local Similarity 86.8%; Pred. No. 7e-17;  
Matches 118; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy      1408 AAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAA 1467
        ||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      223 AAACGAGTTATTTGTTTTGTACAGTCGTGCTTATGCTGCTGGTGCCAATCATTGAAGAA 164

Qy      1468 AAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATAT 1527
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      163 AAACAGTCCTTGGGAAGACAAGCAGTCATGCTTAAAGTTCAAAGCTAATGATCACGGATAT 104

Qy      1528 GACAACTTCCGTTCCA 1543
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      103 GACAACTTCCGTTCCA 88
```

RESULT 13

US-09-120-772-1

; Sequence 1, Application US/09120772

; Patent No. 6143521

; GENERAL INFORMATION:

; APPLICANT: LANE, PAMELA

; APPLICANT: TSUI, PING

; APPLICANT: ELSHOUBAGY, NABIL

; TITLE OF INVENTION: HUMAN BOMBESIN RECEPTOR SUBTYPE

; TITLE OF INVENTION: 3

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ratner & Prestia

; STREET: P.O. Box 980

; CITY: Valley Forge

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/120,772

; FILING DATE: 22-JUL-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Prestia, Paul F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GP-70505

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0700

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1205 base pairs



; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-120-772-1

Query Match 2.5%; Score 106.6; DB 3; Length 1205;  
Best Local Similarity 48.5%; Pred. No. 1.2e-16;  
Matches 425; Conservative 0; Mismatches 434; Indels 18; Gaps 4;

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Qy      578 TGGGGATCATCGGGAAGTCCACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAA 637
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Db      181 TGGGCATCCTTGGAAATGCTATTCTCATCAAAGTCTTTTCAAGACCAAATCCATGCAAA 240

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      | ||| ||||| || ||| ||||| ||||| ||||| || | | | | |
Db      241 CAGTTCCAAATATTTTCATCACCAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACTT 300

Qy      698 ACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGT 757
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Db      301 GTGTGCCAGTGGATGCAACTCACTACCTTGAGAAGGATGGCTGTTCGGAAGAATTGGTT 360

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Db      661 TGTGCTTCTTAGTGTTCTACATTATTCCACTCTCTATTATCTCTGTCTACTATTCTTGA 720

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Db      721 TTGCTAGGACCCTTTACAAAAGCACCTGAACATACCTACTGAGGAACAAAGCCATGCCC 780

Qy      1172 ATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCTGGTCTCTGTCT 1231
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RESULT 14

US-09-016-434-1275

; Sequence 1275, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 1275:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1413 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g291876  
US-09-016-434-1275

Query Match 2.5%; Score 106.6; DB 4; Length 1413;  
Best Local Similarity 48.5%; Pred. No. 1.4e-16;  
Matches 425; Conservative 0; Mismatches 434; Indels 18; Gaps 4;

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Db      328 TGGGCATCCTTGGAAATGCTATTCTCATCAAAGTCTTTTCAAGACCAAATCCATGCAA 387

Qy      638 ACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTG 697
      | ||| ||||| | | | | | | | | | | | | | | | |
Db      388 CAGTTCCAAATATTTTCATCACCAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACTT 447

Qy      698 ACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGT 757
      | || | | ||| | | | | | | | | | | | | | | |
Db      448 GTGTGCCAGTGGATGCAACTCACTACCTGCAGAAGGATGGCTGTTTCGGAAGAATTGGTT 507

Qy      758 GTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTG 817
      ||||| || | ||||| | | | | | | | | | | | | |
Db      508 GTAAGGTGCTCTCTTTCATCCGGCTCACTTCTGTTGGTGTGTCACTGTTTACATTAACAA 567

Qy      818 CTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGG 877
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Db      568 TTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAGCGACAGCCCTCCAATG 627

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Db      628 CCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCGTGTCTATGATATTTGCTC 687

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Qy      993 GCGAATCTGCTTGCT-TCATCCCGTTCAGAAGACAGCTTTCATGCAGTTTTACAAGACAG 1051
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Db      748 TTGAATCATGTACCTCTTATCCTGTCTCTAAGAAGCTCTTGCAAGAAATACATTCTCTGC 807

Qy      1052 CAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTT 1111
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Qy      1112 TTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAA 1171
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Qy      1172 ATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCTGGTCTTGTCT 1231
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Qy      1232 TTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTATAATC 1291
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RESULT 15

US-09-016-434-1215

; Sequence 1215, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 1215:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1726 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GENBANK  
; CLONE: g183649  
US-09-016-434-1215

Query Match 2.5%; Score 106; DB 4; Length 1726;  
Best Local Similarity 52.0%; Pred. No. 2.1e-16;  
Matches 238; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

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Search completed: May 14, 2004, 15:54:40  
Job time : 274.574 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 14, 2004, 10:14:36 ; Search time 1634.24 Seconds  
(without alignments)  
11943.281 Million cell updates/sec

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Perfect score: 4301  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result                      8  
Query

| No.  | Score  | Match | Length | DB | ID                  | Description       |
|------|--------|-------|--------|----|---------------------|-------------------|
| 1    | 4301   | 100.0 | 4301   | 9  | US-09-931-157-2     | Sequence 2, Appli |
| 2    | 4284.4 | 99.6  | 4286   | 10 | US-09-921-406C-13   | Sequence 13, Appl |
| 3    | 4284.4 | 99.6  | 4286   | 15 | US-10-225-567A-113  | Sequence 113, App |
| 4    | 4284.4 | 99.6  | 4286   | 15 | US-10-007-926A-177  | Sequence 177, App |
| 5    | 4284.4 | 99.6  | 4286   | 15 | US-10-210-120-15    | Sequence 15, Appl |
| 6    | 4284.4 | 99.6  | 4286   | 16 | US-10-372-683-48    | Sequence 48, Appl |
| 7    | 4202.4 | 97.7  | 4305   | 13 | US-10-116-802-116   | Sequence 116, App |
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| 9    | 1684.6 | 39.2  | 1892   | 13 | US-10-116-802-117   | Sequence 117, App |
| 10   | 1676.6 | 39.0  | 1877   | 13 | US-10-116-802-118   | Sequence 118, App |
| 11   | 1466.8 | 34.1  | 1470   | 16 | US-10-305-720-1203  | Sequence 1203, Ap |
| 12   | 1389   | 32.3  | 1632   | 12 | US-10-311-671-28    | Sequence 28, Appl |
| 13   | 1322.6 | 30.8  | 1329   | 11 | US-09-826-509-496   | Sequence 496, App |
| 14   | 1220.4 | 28.4  | 1578   | 13 | US-10-235-192A-32   | Sequence 32, Appl |
| 15   | 763.2  | 17.7  | 800    | 9  | US-09-778-927A-27   | Sequence 27, Appl |
| c 16 | 440.6  | 10.2  | 592    | 9  | US-09-962-436-531   | Sequence 531, App |
| c 17 | 440.6  | 10.2  | 592    | 9  | US-09-880-107-2060  | Sequence 2060, Ap |
| c 18 | 440.6  | 10.2  | 592    | 9  | US-09-954-531-917   | Sequence 917, App |
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| 22   | 395.8  | 9.2   | 4105   | 15 | US-10-225-567A-115  | Sequence 115, App |
| 23   | 395.8  | 9.2   | 4105   | 15 | US-10-007-926A-229  | Sequence 229, App |
| 24   | 395.8  | 9.2   | 4105   | 15 | US-10-101-510-370   | Sequence 370, App |
| 25   | 395.8  | 9.2   | 4105   | 16 | US-10-372-683-46    | Sequence 46, Appl |
| 26   | 392.6  | 9.1   | 1284   | 11 | US-09-826-509-494   | Sequence 494, App |
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| c 29 | 302    | 7.0   | 363    | 9  | US-09-954-456-209   | Sequence 209, App |
| c 30 | 302    | 7.0   | 363    | 9  | US-09-954-456-467   | Sequence 467, App |
| c 31 | 302    | 7.0   | 363    | 9  | US-09-954-456-925   | Sequence 925, App |
| c 32 | 302    | 7.0   | 363    | 9  | US-09-954-456-1550  | Sequence 1550, Ap |
| c 33 | 302    | 7.0   | 363    | 9  | US-09-880-107-2076  | Sequence 2076, Ap |
| c 34 | 302    | 7.0   | 363    | 10 | US-09-873-367C-129  | Sequence 129, App |
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| 36   | 152.2  | 3.5   | 6896   | 13 | US-09-854-867-422   | Sequence 422, App |
| 37   | 148.8  | 3.5   | 1889   | 9  | US-09-867-701-10875 | Sequence 10875, A |
| 38   | 147.6  | 3.4   | 3697   | 13 | US-10-363-616-178   | Sequence 178, App |
| c 39 | 144    | 3.3   | 60381  | 13 | US-10-087-192-970   | Sequence 970, App |
| 40   | 131.6  | 3.1   | 1330   | 10 | US-09-374-046A-151  | Sequence 151, App |
| 41   | 131.6  | 3.1   | 1330   | 13 | US-10-616-263-151   | Sequence 151, App |
| 42   | 131    | 3.0   | 7813   | 13 | US-09-854-867-27    | Sequence 27, Appl |
| c 43 | 128.4  | 3.0   | 503    | 15 | US-10-264-283-84    | Sequence 84, Appl |
| c 44 | 128.4  | 3.0   | 738    | 13 | US-10-276-774-868   | Sequence 868, App |
| 45   | 128.4  | 3.0   | 858    | 15 | US-10-198-846-12892 | Sequence 12892, A |

#### ALIGNMENTS

##### RESULT 1

US-09-931-157-2

; Sequence 2, Application US/09931157

; Patent No. US20020082414A1

; GENERAL INFORMATION:

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; APPLICANT: Imura, Hiroo
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Nakanishi, Shigetada
; TITLE OF INVENTION: Human Endothelin Receptor
; FILE REFERENCE: 299002032411
; CURRENT APPLICATION NUMBER: US/09/931,157
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 08/121,446
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: 07/911,684
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: JP 3-172828
; PRIOR FILING DATE: 1991-07-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4301
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (238)...(1566)
US-09-931-157-2

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Query Match          100.0%; Score 4301; DB 9; Length 4301;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCGCTGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCGCTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

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|    |      |  |      |
|----|------|--|------|
| Db | 421  | <br>CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG   | 480  |
| Qy | 481  | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA      | 540  |
| Db | 481  | <br>CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA  | 540  |
| Qy | 541  | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA     | 600  |
| Db | 541  | <br>TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA | 600  |
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC       | 660  |
| Db | 601  | <br>CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Qy | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG       | 720  |
| Db | 661  | <br>AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG       | 780  |
| Db | 721  | <br>CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA       | 840  |
| Db | 781  | <br>AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA       | 900  |
| Db | 841  | <br>GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT       | 960  |
| Db | 901  | <br>ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG      | 1020 |
| Db | 961  | <br>ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT      | 1080 |
| Db | 1021 | <br>AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT  | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG      | 1140 |
| Db | 1081 | <br>TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG       | 1200 |
| Db | 1141 | <br>AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC       | 1260 |
| Db | 1201 | <br>GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG      | 1320 |
|    |      |  |      |

|    |      |  |      |
|----|------|--|------|
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
|    |      |  |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAAGATTCAAAAAGCTGCTTTAAGTCATGCTTA | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAAGATTCAAAAAGCTGCTTTAAGTCATGCTTA | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGCTTA    | 1500 |
|    |      |  |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGCTCA  | 1560 |
|    |      |  |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGCTCA  | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAAGCTATTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
|    |      |  |      |
| Db | 1561 | TCTTGAAAGAAGAAGCTATTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAGCTATGTATTTGCACAGCACACTAT    | 1680 |
|    |      |  |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAGCTATGTATTTGCACAGCACACTAT    | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
|    |      |  |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
|    |      |  |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
|    |      |  |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAGAGATTTATTTTTA    | 1920 |
|    |      |  |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAGAGATTTATTTTTA    | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG   | 1980 |
|    |      |  |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT     | 2040 |
|    |      |  |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT     | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
|    |      |  |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
|    |      |  |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |

|    |      |  |      |
|----|------|--|------|
| Qy | 2161 | TTTTGAAAATCATTACACTTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
|    |      |  |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA   | 2280 |
|    |      |  |      |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA   | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA    | 2340 |
|    |      |  |      |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA    | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA    | 2400 |
|    |      |  |      |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA    | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTT    | 2460 |
|    |      |  |      |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTT    | 2460 |
| Qy | 2461 | TCCTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA    | 2520 |
|    |      |  |      |
| Db | 2461 | TCCTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA    | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
|    |      |  |      |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
|    |      |  |      |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTCACCCTATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT  | 2700 |
|    |      |  |      |
| Db | 2641 | GCAGGTAGCACCCCTCTCTCACCCTATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT  | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG    | 2760 |
|    |      |  |      |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG    | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
|    |      |  |      |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT    | 2880 |
|    |      |  |      |
| Db | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT    | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
|    |      |  |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
|    |      |  |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |

|    |      |  |      |
|----|------|--|------|
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTGTCATTGCCT   | 3060 |
|    |      |  |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTGTCATTGCCT   | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
|    |      |  |      |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA  | 3180 |
|    |      |  |      |
| Db | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA  | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
|    |      |  |      |
| Db | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA    | 3300 |
|    |      |  |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA    | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
|    |      |  |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA    | 3480 |
|    |      |  |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA    | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA   | 3540 |
|    |      |  |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA   | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCCTTCTCCATGTGAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
|    |      |  |      |
| Db | 3541 | TCCTGATACCCTTTCCTTCTCCATGTGAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT  | 3660 |
|    |      |  |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT  | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT     | 3720 |
|    |      |  |      |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT     | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT   | 3780 |
|    |      |  |      |
| Db | 3721 | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT   | 3780 |
| Qy | 3781 | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
|    |      |  |      |
| Db | 3781 | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT   | 3900 |

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Db      3841  |||||CAGCTCAAAAAGATTTATAAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900
Qy      3901  GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
Db      3901  |||||GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
Qy      3961  GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAAGTGTAATATAACAATGT 4020
Db      3961  |||||GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAAGTGTAATATAACAATGT 4020
Qy      4021  AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
Db      4021  |||||AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
Qy      4081  TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAAACAACCTACCTATTTTTTC 4140
Db      4081  |||||TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAAACAACCTACCTATTTTTTC 4140
Qy      4141  ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAAATGTGA 4200
Db      4141  |||||ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAAATGTGA 4200
Qy      4201  CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
Db      4201  |||||CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
Qy      4261  AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301
Db      4261  |||||AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301

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RESULT 2

US-09-921-406C-13

; Sequence 13, Application US/09921406C

; Publication No. US20030152923A1

; GENERAL INFORMATION:

; APPLICANT: Yakhini, Zohar

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; TITLE OF INVENTION: Classifying Cancers

; FILE REFERENCE: 10010313-1

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; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 4286

; TYPE: DNA

; ORGANISM: Homo sapiens

Query Match 99.6%; Score 4284.4; DB 10; Length 4286;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC   | 60  |
|    |     |   |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC   | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
|    |     |   |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGAGTCTGGACATCTGA   | 180 |
|    |     |   |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGAGTCTGGACATCTGA   | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
|    |     |   |     |
| Db | 181 | AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300 |
|    |     |   |     |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
|    |     |   |     |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
|    |     |   |     |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
| Qy | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
|    |     |   |     |
| Db | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540 |
|    |     |   |     |
| Db | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540 |
| Qy | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA | 600 |
|    |     |   |     |
| Db | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA | 600 |
| Qy | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
|    |     |   |     |
| Db | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
| Qy | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
|    |     |   |     |
| Db | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
| Qy | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |
|    |     |   |     |
| Db | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |

|    |      |   |      |
|----|------|---|------|
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
|    |      |   |      |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
|    |      |   |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTGAT | 960  |
|    |      |   |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTGAT | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
|    |      |   |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTACAAGACAGCAAAAGATTGGTGGCTGTTGAGTTTCTAT   | 1080 |
|    |      |   |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTACAAGACAGCAAAAGATTGGTGGCTGTTGAGTTTCTAT   | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG | 1140 |
|    |      |   |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
|    |      |   |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
|    |      |   |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
|    |      |   |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
|    |      |   |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
|    |      |   |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
|    |      |   |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
|    |      |   |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA      | 1620 |
|    |      |   |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA      | 1620 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT  | 1680 |
|    |      |   |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT  | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
|    |      |   |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTACACAACACT   | 1860 |
|    |      |   |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTACACAACACT   | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA | 1920 |
|    |      |   |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
|    |      |   |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
|    |      |   |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
|    |      |   |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC   | 2220 |
|    |      |   |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTTACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC   | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
|    |      |   |      |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
|    |      |   |      |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
|    |      |   |      |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTTT   | 2460 |
|    |      |   |      |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTTT   | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |



|    |      |   |      |
|----|------|---|------|
| Db | 2461 | <br>TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT      | 2580 |
| Db | 2521 | <br>CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG      | 2640 |
| Db | 2581 | <br>GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT     | 2700 |
| Db | 2641 | <br>GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG       | 2760 |
| Db | 2701 | <br>GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG      | 2820 |
| Db | 2761 | <br>TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT       | 2880 |
| Db | 2821 | <br>ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT   | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT      | 2940 |
| Db | 2881 | <br>AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG      | 3000 |
| Db | 2941 | <br>GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT     | 3060 |
| Db | 3001 | <br>GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA        | 3120 |
| Db | 3061 | <br>CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA      | 3180 |
| Db | 3121 | <br>GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA  | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG      | 3240 |
| Db | 3181 | <br>ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG  | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA        | 3300 |
| Db | 3241 | <br>TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA    | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC      | 3360 |
|    |      |   |      |

|    |      |   |      |
|----|------|---|------|
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
| Qy | 3361 | ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |   |      |
| Db | 3361 | ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
|    |      |   |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA  | 3540 |
|    |      |   |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA  | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
|    |      |   |      |
| Db | 3541 | TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
| Qy | 3601 | TGAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT   | 3660 |
|    |      |   |      |
| Db | 3601 | TGAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT   | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
|    |      |   |      |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
|    |      |   |      |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
| Qy | 3781 | TTCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
|    |      |   |      |
| Db | 3781 | TTCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
|    |      |   |      |
| Db | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
|    |      |   |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
|    |      |   |      |
| Db | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
|    |      |   |      |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAAACACTACCTTATTTTTTC  | 4140 |
|    |      |   |      |
| Db | 4081 | TTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAAACACTACCTTATTTTTTC  | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA  | 4200 |
|    |      |   |      |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA  | 4200 |

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Qy      4201 CAAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
          |||
Db      4201 CAAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260

Qy      4261 AAAATGCCACATTTCTGGTCTCTGGG 4286
          |||
Db      4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

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RESULT 3

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; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

; FILE REFERENCE: 1920-4-4

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; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 113

; LENGTH: 4286

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-113

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Query Match          99.6%; Score 4284.4; DB 15; Length 4286;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60
          |||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy      61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCGGCTGG 120
          |||
Db      61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCGGCTGG 120

Qy      121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
          |||
Db      121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy      181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
          |||
Db      181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy      241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300
          |||
Db      241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

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|    |      |  |      |
|----|------|--|------|
| Qy | 301  | TCGCGGATCTGGGGAGAGGAGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA | 360  |
|    |      |  |      |
| Db | 301  | TCGCGGATCTGGGGAGAGGAGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA | 360  |
| Qy | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 420  |
|    |      |  |      |
| Db | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 420  |
| Qy | 421  | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG   | 480  |
|    |      |  |      |
| Db | 421  | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG   | 480  |
| Qy | 481  | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540  |
|    |      |  |      |
| Db | 481  | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540  |
| Qy | 541  | TACATCAACACGGTTGTGTCTGCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA   | 600  |
|    |      |  |      |
| Db | 541  | TACATCAACACGGTTGTGTCTGCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA   | 600  |
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
|    |      |  |      |
| Db | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Qy | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
|    |      |  |      |
| Db | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
|    |      |  |      |
| Db | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
|    |      |  |      |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
|    |      |  |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
|    |      |  |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
|    |      |  |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAATTTCTAT | 1080 |
|    |      |  |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAATTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
|    |      |  |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
|    |      |   |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
|    |      |   |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG | 1320 |
|    |      |   |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG | 1320 |
| Qy | 1321 | AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
|    |      |   |      |
| Db | 1321 | AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA    | 1440 |
|    |      |   |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
|    |      |   |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
|    |      |   |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA  | 1620 |
|    |      |   |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA  | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAAGCTATGTATTTGCACAGCACACTAT | 1680 |
|    |      |   |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAAGCTATGTATTTGCACAGCACACTAT | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT    | 1740 |
|    |      |   |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT    | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAAGCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAAGCTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA  | 1920 |
|    |      |   |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA  | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
|    |      |   |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAAGCTTTTCAATTAATAT    | 2040 |

|    |      |   |      |
|----|------|---|------|
| Db | 1981 | <br>AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT      | 2100 |
| Db | 2041 | <br>TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT      | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC      | 2220 |
| Db | 2161 | <br>TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA      | 2280 |
| Db | 2221 | <br>CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA       | 2340 |
| Db | 2281 | <br>TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA       | 2400 |
| Db | 2341 | <br>CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTT       | 2460 |
| Db | 2401 | <br>CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTT   | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA      | 2520 |
| Db | 2461 | <br>TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT      | 2580 |
| Db | 2521 | <br>CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG      | 2640 |
| Db | 2581 | <br>GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Qy | 2641 | GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT       | 2700 |
| Db | 2641 | <br>GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT   | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG       | 2760 |
| Db | 2701 | <br>GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG      | 2820 |
| Db | 2761 | <br>TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCCAAACTGCTTTTTGAGACCGTAAGAACCTCTT      | 2880 |
|    |      |   |      |

Db 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
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 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 Qy 3061 CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
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 Db 3061 CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 Qy 3121 GAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA 3180  
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 Db 3121 GAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA 3180  
 Qy 3181 ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAATAAGCTAGTAATG 3240  
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 Db 3181 ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAATAAGCTAGTAATG 3240  
 Qy 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
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 Db 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
 Qy 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 Qy 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
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 Db 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 Qy 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA 3540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA 3540  
 Qy 3541 TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
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 Db 3541 TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 Qy 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAAATTGCATTCACTGGCTT 3660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAAATTGCATTCACTGGCTT 3660  
 Qy 3661 TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3661 TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720

Qy 3721 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3721 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780  
 Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 Qy 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 Qy 3961 GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGAATATAACAATGT 4020  
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 Db 3961 GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGAATATAACAATGT 4020  
 Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 Qy 4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTTTAACAACTACCTTATTTTTC 4140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTTTAACAACTACCTTATTTTTC 4140  
 Qy 4141 ACTGTACAGACACTAATTCATTAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4141 ACTGTACAGACACTAATTCATTAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
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 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 4

US-10-007-926A-177

; Sequence 177, Application US/10007926A

; Publication No. US20030143539A1

; GENERAL INFORMATION:

; APPLICANT: BERTUCCI, FRANCOIS

; APPLICANT: HOULGATTE, REMI

; APPLICANT: BIRNBAUM, DANIEL

; APPLICANT: NGUYEN, CATHERINE

; APPLICANT: VIENS, PATRICE

; APPLICANT: FERT, VINCENT

; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS

; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

; FILE REFERENCE: 1546-R-00

; CURRENT APPLICATION NUMBER: US/10/007,926A



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; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 177
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: endothelin receptor type b (EDNRB) gene.
US-10-007-926A-177
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Query Match          99.6%; Score 4284.4; DB 15; Length 4286;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA 540

Qy    541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA 600
```

Qy 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 |||  
 Db 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660

Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 |||  
 Db 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720

Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 |||  
 Db 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780

Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840

Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 |||  
 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900

Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 |||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960

Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020  
 |||  
 Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020

Qy 1021 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCACTTTCTAT 1080  
 |||  
 Db 1021 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCACTTTCTAT 1080

Qy 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 |||  
 Db 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG 1140

Qy 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 |||  
 Db 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200

Qy 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260  
 |||  
 Db 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260

Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG 1320  
 |||  
 Db 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG 1320

Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 |||  
 Db 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380

Qy 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA 1440  
 |||  
 Db 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA 1440

Qy 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500

|    |      |  |      |
|----|------|--|------|
| Db | 1441 | <br>TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA       | 1560 |
| Db | 1501 | <br>AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA           | 1620 |
| Db | 1561 | <br>TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA       | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAACACTATGTATTTGCACAGCACACTAT       | 1680 |
| Db | 1621 | <br>AACAAAATGAAACATTTGCCAAAACAAAACAAAACACTATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAAATATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT     | 1740 |
| Db | 1681 | <br>TAAAAATATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT       | 1800 |
| Db | 1741 | <br>TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT       | 1860 |
| Db | 1801 | <br>TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT         | 1920 |
| Db | 1861 | <br>TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT     | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACCTTTTAAATG      | 1980 |
| Db | 1921 | <br>AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACCTTTTAAATG  | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT         | 2040 |
| Db | 1981 | <br>AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT     | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT       | 2100 |
| Db | 2041 | <br>TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT       | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC       | 2220 |
| Db | 2161 | <br>TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC   | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA       | 2280 |
| Db | 2221 | <br>CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA   | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTAAACCTCA             | 2340 |
|    |      |  |      |

Db 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA 2340  
 Qy 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA 2400  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA 2400  
 Qy 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT 2460  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT 2460  
 Qy 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 Qy 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Qy 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Qy 2641 GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2641 GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 Qy 2701 GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2701 GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760  
 Qy 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 Qy 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 Qy 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 Qy 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180

|    |      |  |      |
|----|------|--|------|
| Qy | 3181 | ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
|    |      |  |      |
| Db | 3181 | ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA   | 3300 |
|    |      |  |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA   | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC | 3360 |
|    |      |  |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC | 3360 |
| Qy | 3361 | ACAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 3361 | ACAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA | 3480 |
|    |      |  |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA   | 3540 |
|    |      |  |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA   | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
|    |      |  |      |
| Db | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
| Qy | 3601 | TGAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT   | 3660 |
|    |      |  |      |
| Db | 3601 | TGAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT   | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT  | 3720 |
|    |      |  |      |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT  | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCACTTCAAACATGT    | 3780 |
|    |      |  |      |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCACTTCAAACATGT    | 3780 |
| Qy | 3781 | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
|    |      |  |      |
| Db | 3781 | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT | 3900 |
|    |      |  |      |
| Db | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
|    |      |  |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT | 4020 |
|    |      |  |      |
| Db | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT | 4020 |

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 |||  
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 Qy 4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140  
 |||  
 Db 4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140  
 Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200  
 |||  
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200  
 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 |||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 |||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

# RESULT 5

US-10-210-120-15

; Sequence 15, Application US/10210120  
 ; Publication No. US20030175736A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chinnaiyan, Arul M.  
 ; APPLICANT: Rubin, Mark A.  
 ; APPLICANT: Sreekumar, Arun  
 ; TITLE OF INVENTION: Expression Profile of Prostate Cancer  
 ; FILE REFERENCE: UM-07221  
 ; CURRENT APPLICATION NUMBER: US/10/210,120  
 ; CURRENT FILING DATE: 2002-08-01  
 ; PRIOR APPLICATION NUMBER: US 60/309,581  
 ; PRIOR FILING DATE: 2001-08-02  
 ; PRIOR APPLICATION NUMBER: US 60/334,468  
 ; PRIOR FILING DATE: 2001-11-15  
 ; NUMBER OF SEQ ID NOS: 123  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 15  
 ; LENGTH: 4286  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-210-120-15

Query Match 99.6%; Score 4284.4; DB 15; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60  
 |||  
 Db 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60  
 Qy 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120  
 |||  
 Db 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180  
 |||  
 Db 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180

Qy 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
 |||  
 Db 181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300  
 |||  
 Db 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

Qy 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360  
 |||  
 Db 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420  
 |||  
 Db 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy 421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
 |||  
 Db 421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540  
 |||  
 Db 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540

Qy 541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTGCTGGGGATCATCGGGAAGTCCACA 600  
 |||  
 Db 541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTGCTGGGGATCATCGGGAAGTCCACA 600

Qy 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 |||  
 Db 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660

Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 |||  
 Db 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720

Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 |||  
 Db 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780

Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840

Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 |||  
 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900

Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 |||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960

Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020

|    |      |  |      |
|----|------|--|------|
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
| Qy | 1021 | AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Db | 1021 | AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCACTTTCTTTATATTGGACCGAAGTCATTAA  | 1620 |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCACTTTCTTTATATTGGACCGAAGTCATTAA  | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |



Db 1801 TTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT 1860  
 Qy 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT 1920  
 Db 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT 1920  
 Qy 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG 1980  
 Db 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG 1980  
 Qy 1981 AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT 2040  
 Db 1981 AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT 2040  
 Qy 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT 2100  
 Db 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT 2100  
 Qy 2101 TTTTCGGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT 2160  
 Db 2101 TTTTCGGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT 2160  
 Qy 2161 TTTTGAAAATCATTACACTTTTCTAGTAAGCCCAAACCTCAGCATTCTGCAATATGTAAC 2220  
 Db 2161 TTTTGAAAATCATTACACTTTTCTAGTAAGCCCAAACCTCAGCATTCTGCAATATGTAAC 2220  
 Qy 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA 2280  
 Db 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA 2280  
 Qy 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA 2340  
 Db 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA 2340  
 Qy 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA 2400  
 Db 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA 2400  
 Qy 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTT 2460  
 Db 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTT 2460  
 Qy 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 Db 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 Qy 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Db 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Qy 2581 GCCAGTGACCTCATAATAAGACTGTGAAGCTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Db 2581 GCCAGTGACCTCATAATAAGACTGTGAAGCTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Qy 2641 GCAGGTAGCACCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 Db 2641 GCAGGTAGCACCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700

Qy 2701 GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760  
 |||  
 Db 2701 GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760

Qy 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 |||  
 Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820

Qy 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT 2880  
 |||  
 Db 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT 2880

Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 |||  
 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940

Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 |||  
 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000

Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 |||  
 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTTCGTCATTGCCT 3060

Qy 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 |||  
 Db 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120

Qy 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA 3180  
 |||  
 Db 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA 3180

Qy 3181 ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 |||  
 Db 3181 ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240

Qy 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
 |||  
 Db 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300

Qy 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 |||  
 Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360

Qy 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 |||  
 Db 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420

Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 |||  
 Db 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480

Qy 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA 3540  
 |||  
 Db 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA 3540

|    |      |   |      |
|----|------|---|------|
| Qy | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
|    |      |   |      |
| Db | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
|    |      |   |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
|    |      |   |      |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT  | 3780 |
|    |      |   |      |
| Db | 3721 | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT  | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAAATTATTGTTAACATGGATGTTA | 3840 |
|    |      |   |      |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAAATTATTGTTAACATGGATGTTA | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
|    |      |   |      |
| Db | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
|    |      |   |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
|    |      |   |      |
| Db | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
|    |      |   |      |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC     | 4140 |
|    |      |   |      |
| Db | 4081 | TTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC     | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA  | 4200 |
|    |      |   |      |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA  | 4200 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT  | 4260 |
|    |      |   |      |
| Db | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT  | 4260 |
| Qy | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                    | 4286 |
|    |      |   |      |
| Db | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                    | 4286 |

RESULT 6

US-10-372-683-48

; Sequence 48, Application US/10372683

; Publication No. US20040009171A1

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; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: PEALE JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 48
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-372-683-48
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Query Match          99.6%; Score 4284.4; DB 16; Length 4286;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
        |||||||
Db       1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

QY      61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
        |||||||
Db       61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

QY     121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
        |||||||
Db     121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

QY     181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
        |||||||
Db     181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

QY     241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300
        |||||||
Db     241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

QY     301 TCGCGGATCTGGGGAGAGGAGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
        |||||||
Db     301 TCGCGGATCTGGGGAGAGGAGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

QY     361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
        |||||||
Db     361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

QY     421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
        |||||||
Db     421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

QY     481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540
        |||||||
```

Db 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540  
 Qy 541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA 600  
 Qy 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCCTTCAG 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCCTTCAG 1020  
 Qy 1021 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1021 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080  
 Qy 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 Qy 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 Qy 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260  
 Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTG 1320  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTG 1320  
 Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380

|    |      |  |      |
|----|------|--|------|
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
|    |      |  |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
|    |      |  |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTTCACTGTATTTTCTTTATATTGGACCGAAGTCATTAA       | 1620 |
|    |      |  |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTTCACTGTATTTTCTTTATATTGGACCGAAGTCATTAA       | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAACATATGTATTTGCACAGCACACTAT    | 1680 |
|    |      |  |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAACATATGTATTTGCACAGCACACTAT    | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTAACACTCACAGCTACATATGACATTTTATGAGCTGT    | 1740 |
|    |      |  |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTAACACTCACAGCTACATATGACATTTTATGAGCTGT    | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
|    |      |  |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
|    |      |  |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
| Qy | 1861 | TAGGCTTAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAGAGATTTATTTTTTA    | 1920 |
|    |      |  |      |
| Db | 1861 | TAGGCTTAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAGAGATTTATTTTTTA    | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG   | 1980 |
|    |      |  |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT     | 2040 |
|    |      |  |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT     | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
|    |      |  |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
|    |      |  |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTCACTAGAAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
|    |      |  |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTTCACTAGAAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |

Qy 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA 2280  
 |||  
 Db 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA 2280

Qy 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA 2340  
 |||  
 Db 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA 2340

Qy 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTGAATCTGTCATTCA 2400  
 |||  
 Db 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTGAATCTGTCATTCA 2400

Qy 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTTT 2460  
 |||  
 Db 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTTT 2460

Qy 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 |||  
 Db 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520

Qy 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 |||  
 Db 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580

Qy 2581 GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 |||  
 Db 2581 GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640

Qy 2641 GCAGGTAGCACCCTCTCTCACCCTATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT 2700  
 |||  
 Db 2641 GCAGGTAGCACCCTCTCTCACCCTATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT 2700

Qy 2701 GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG 2760  
 |||  
 Db 2701 GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG 2760

Qy 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 |||  
 Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820

Qy 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 |||  
 Db 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880

Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 |||  
 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940

Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 |||  
 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000

Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTCGTCATTGCCT 3060  
 |||  
 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTCGTCATTGCCT 3060

Qy 3061 CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAACACAGTGCAATGTTCTCA 3120

|    |      |  |   |      |
|----|------|--|---|------|
| Db | 3061 |  | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |
| Qy | 3121 |  | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA   | 3180 |
| Db | 3121 |  | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA   | 3180 |
| Qy | 3181 |  | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
| Db | 3181 |  | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
| Qy | 3241 |  | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA   | 3300 |
| Db | 3241 |  | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA   | 3300 |
| Qy | 3301 |  | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
| Db | 3301 |  | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
| Qy | 3361 |  | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Db | 3361 |  | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 |  | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
| Db | 3421 |  | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
| Qy | 3481 |  | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA  | 3540 |
| Db | 3481 |  | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA  | 3540 |
| Qy | 3541 |  | TCCTGATACCCTTTCTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT    | 3600 |
| Db | 3541 |  | TCCTGATACCCTTTCTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT    | 3600 |
| Qy | 3601 |  | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT  | 3660 |
| Db | 3601 |  | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT  | 3660 |
| Qy | 3661 |  | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Db | 3661 |  | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Qy | 3721 |  | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT  | 3780 |
| Db | 3721 |  | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT  | 3780 |
| Qy | 3781 |  | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
| Db | 3781 |  | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
| Qy | 3841 |  | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Db | 3841 |  | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Qy | 3901 |  | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
|    |      |  |   |      |



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Db      3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
Qy      3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAAGTGTAAATATAACAATGT 4020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAAGTGTAAATATAACAATGT 4020
Qy      4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
Qy      4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 4140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 4140
Qy      4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200
Qy      4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
Qy      4261 AAAATGCCACATTTCTGGTCTCTGGG 4286
        ||||||||||||||||||
Db      4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

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RESULT 7

US-10-116-802-116

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; Sequence 116, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 116
; LENGTH: 4305
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 1094000.4
; NAME/KEY: unsure
; LOCATION: 4301-4302
; OTHER INFORMATION: a, t, c, g, or other
US-10-116-802-116

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Query Match          97.7%; Score 4202.4; DB 13; Length 4305;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 4280; Conservative 0; Mismatches 18; Indels 8; Gaps 6;

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Qy 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60  
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 Db 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120  
 |||||  
 Db 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180  
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 Db 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
 |||||  
 Db 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300  
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 Db 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300

Qy 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360  
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 Db 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420  
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 Db 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
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 Db 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540  
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 Db 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540

Qy 541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA 600  
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 Db 541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA 600

Qy 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 |||||  
 Db 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660

Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 |||||  
 Db 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720

Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 780  
 |||||  
 Db 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 780

Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840

Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900

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|----|------|--|------|
| Db | 841  | <br>GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAATGGACAGCAGTAGAA    | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT       | 960  |
| Db | 901  | <br>ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG       | 1020 |
| Db | 961  | <br>ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
| Qy | 1021 | AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT     | 1080 |
| Db | 1021 | <br>AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG       | 1140 |
| Db | 1081 | <br>TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG       | 1200 |
| Db | 1141 | <br>AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC        | 1260 |
| Db | 1201 | <br>GCCAAAACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC    | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG       | 1320 |
| Db | 1261 | <br>AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT       | 1380 |
| Db | 1321 | <br>AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA        | 1440 |
| Db | 1381 | <br>AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA       | 1500 |
| Db | 1441 | <br>TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA        | 1560 |
| Db | 1501 | <br>AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACCGAAGTCATTAA            | 1620 |
| Db | 1561 | <br>TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACCGAAGTCATTAA        | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT       | 1680 |
| Db | 1621 | <br>AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT       | 1740 |
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| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT    | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
|    |      |   |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG    | 1980 |
|    |      |   |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG    | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTTTCAATTAATAT     | 2040 |
|    |      |   |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTTTCAATTAATAT     | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT | 2160 |
|    |      |   |      |
| Db | 2101 | TTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTAC--TAGAAGCCCAAACCTCAGCATT-CTGCAATATGT  | 2217 |
|    |      |   |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTTACCTAGAAGCCCAAACCTCAGCATTCTGCAATATGT    | 2220 |
| Qy | 2218 | AA-CCAACATGTCACAAACAAGCAG--CATGTAACAGACTGGCACATGTG-CCAGCTGAA  | 2273 |
|    |      |   |      |
| Db | 2221 | AACCCAACATGTCACAAACAAGCCAGCCATGTAACAGACTGGCACATGTGCCAGCTGAA   | 2280 |
| Qy | 2274 | TTTAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCA  | 2333 |
|    |      |   |      |
| Db | 2281 | TTTAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCA  | 2340 |
| Qy | 2334 | AACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTG   | 2393 |
|    |      |   |      |
| Db | 2341 | AACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTG   | 2400 |
| Qy | 2394 | TCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCT  | 2453 |
|    |      |   |      |
| Db | 2401 | TCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCT  | 2460 |
| Qy | 2454 | TCTTTTTTCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCT   | 2513 |
|    |      |   |      |
| Db | 2461 | TCTTCTTCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCT    | 2520 |
| Qy | 2514 | ACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATG  | 2573 |
|    |      |   |      |
| Db | 2521 | ACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATG  | 2580 |

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|----|------|---|------|
| Qy | 2574 | GAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGA  | 2633 |
|    |      |   |      |
| Db | 2581 | GAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGA  | 2640 |
| Qy | 2634 | CAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATAT | 2693 |
|    |      |   |      |
| Db | 2641 | CAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATAT | 2700 |
| Qy | 2694 | GTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAG   | 2753 |
|    |      |   |      |
| Db | 2701 | GTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAG   | 2760 |
| Qy | 2754 | CTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGT  | 2813 |
|    |      |   |      |
| Db | 2761 | CTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGT  | 2820 |
| Qy | 2814 | TTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAAACGCTTTTGTAGACCGTAAGA   | 2873 |
|    |      |   |      |
| Db | 2821 | TTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAAACGCTTTTGTAGACCGTAAGA   | 2880 |
| Qy | 2874 | ACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGG  | 2933 |
|    |      |   |      |
| Db | 2881 | ACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGG  | 2940 |
| Qy | 2934 | ATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAA  | 2993 |
|    |      |   |      |
| Db | 2941 | ATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAA  | 3000 |
| Qy | 2994 | TGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATCCCATTCTTAGCCTAACGTTTCGTC  | 3053 |
|    |      |   |      |
| Db | 3001 | TGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATCCCATTCTTAGCCTAACGTTTCGTC  | 3060 |
| Qy | 3054 | ATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAACACAGTGCAAT    | 3113 |
|    |      |   |      |
| Db | 3061 | ATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAACACAGTGCAAT    | 3120 |
| Qy | 3114 | GTTCTCAGAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATA   | 3173 |
|    |      |   |      |
| Db | 3121 | GTTCTCAGAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATA   | 3180 |
| Qy | 3174 | TGCCCAAATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCT   | 3233 |
|    |      |   |      |
| Db | 3181 | TGCCCAAATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCT   | 3240 |
| Qy | 3234 | AGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAAT    | 3293 |
|    |      |   |      |
| Db | 3241 | AGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAAT    | 3300 |
| Qy | 3294 | GTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAA  | 3353 |
|    |      |   |      |
| Db | 3301 | GTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAA  | 3360 |
| Qy | 3354 | ATCACCCACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCA | 3413 |
|    |      |   |      |
| Db | 3361 | ATCACCCACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCA | 3420 |

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| Qy | 3414 | TAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGT  | 3473 |
|    |      |   |      |
| Db | 3421 | TAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGT  | 3480 |
| Qy | 3474 | TTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAAT   | 3533 |
|    |      |   |      |
| Db | 3481 | TTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAAT   | 3540 |
| Qy | 3534 | TTTACATCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGC  | 3593 |
|    |      |   |      |
| Db | 3541 | TTTACATCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGC  | 3600 |
| Qy | 3594 | CAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAAATTGCATTCA | 3653 |
|    |      |   |      |
| Db | 3601 | CAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAAATTGCATTCA | 3660 |
| Qy | 3654 | GTGGCTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAA     | 3713 |
|    |      |   |      |
| Db | 3661 | GTGGCTTTT-AAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAA    | 3719 |
| Qy | 3714 | TTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAA   | 3773 |
|    |      |   |      |
| Db | 3720 | TTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAA   | 3779 |
| Qy | 3774 | AACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATG  | 3833 |
|    |      |   |      |
| Db | 3780 | AACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATG  | 3839 |
| Qy | 3834 | GATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCAC   | 3893 |
|    |      |   |      |
| Db | 3840 | GATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCAC   | 3899 |
| Qy | 3894 | TGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAG  | 3953 |
|    |      |   |      |
| Db | 3900 | TGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAG  | 3959 |
| Qy | 3954 | GAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATA  | 4013 |
|    |      |   |      |
| Db | 3960 | GAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATA  | 4019 |
| Qy | 4014 | ACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTA  | 4073 |
|    |      |   |      |
| Db | 4020 | ACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTA  | 4079 |
| Qy | 4074 | CTGATTTTTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTT     | 4133 |
|    |      |   |      |
| Db | 4080 | CTGATTTTTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTT     | 4139 |
| Qy | 4134 | ATTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATA   | 4193 |
|    |      |   |      |
| Db | 4140 | ATTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATA   | 4199 |
| Qy | 4194 | AATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTA  | 4253 |
|    |      |   |      |
| Db | 4200 | AATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTA  | 4259 |
| Qy | 4254 | TTCAATTAAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAA                | 4299 |

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| Qy | 1430  | AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC  | 1489  |
| Db | 72830 | AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC  | 72771 |
| Qy | 1490  | AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA  | 1549  |
| Db | 72770 | AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA  | 72711 |
| Qy | 1550  | AATACAGCTCATCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACC  | 1609  |
| Db | 72710 | AATACAGCTCATCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACC  | 72651 |
| Qy | 1610  | GAAGTCATTAAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA | 1669  |
| Db | 72650 | GAAGTCATTAAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA | 72591 |
| Qy | 1670  | CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT | 1729  |
| Db | 72590 | CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT | 72531 |
| Qy | 1730  | TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA  | 1789  |
| Db | 72530 | TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA  | 72471 |
| Qy | 1790  | AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT  | 1849  |

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|----|-------|--|-------|
| Db | 72470 | AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATT   | 72411 |
| Qy | 1850  | CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG   | 1909  |
|    |       |  |       |
| Db | 72410 | CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG   | 72351 |
| Qy | 1910  | ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGA | 1969  |
|    |       |  |       |
| Db | 72350 | ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGA | 72291 |
| Qy | 1970  | ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAACAACCTTT   | 2029  |
|    |       |  |       |
| Db | 72290 | ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAACAACCTTT   | 72231 |
| Qy | 2030  | TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT   | 2089  |
|    |       |  |       |
| Db | 72230 | TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT   | 72171 |
| Qy | 2090  | AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG | 2149  |
|    |       |  |       |
| Db | 72170 | AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG | 72111 |
| Qy | 2150  | AGCAAGGCTGTTTTTGAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTG    | 2209  |
|    |       |  |       |
| Db | 72110 | AGCAAGGCTGTTTTTGAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTG    | 72051 |
| Qy | 2210  | CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC   | 2269  |
|    |       |  |       |
| Db | 72050 | CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC   | 71991 |
| Qy | 2270  | TGAATTTAAATATAATACTTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG  | 2329  |
|    |       |  |       |
| Db | 71990 | TGAATTTAAATATAATACTTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG  | 71931 |
| Qy | 2330  | ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA    | 2389  |
|    |       |  |       |
| Db | 71930 | ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA    | 71871 |
| Qy | 2390  | TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAA   | 2449  |
|    |       |  |       |
| Db | 71870 | TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAA   | 71811 |
| Qy | 2450  | ATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT   | 2509  |
|    |       |  |       |
| Db | 71810 | ATCTTCTTCTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT   | 71751 |
| Qy | 2510  | ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC   | 2569  |
|    |       |  |       |
| Db | 71750 | ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC   | 71691 |
| Qy | 2570  | GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC   | 2629  |
|    |       |  |       |
| Db | 71690 | GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC   | 71631 |
| Qy | 2630  | ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC   | 2689  |
|    |       |  |       |
| Db | 71630 | ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC   | 71571 |



|    |       |  |       |
|----|-------|--|-------|
| Qy | 2690  | ATATGTATAATGCTATAGTTAAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTA | 2749  |
|    |       |  |       |
| Db | 71570 | ATATGTATAATGCTATAGTTAAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTA | 71511 |
| Qy | 2750  | ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA   | 2809  |
|    |       |  |       |
| Db | 71510 | ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA   | 71451 |
| Qy | 2810  | AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT    | 2869  |
|    |       |  |       |
| Db | 71450 | AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT    | 71391 |
| Qy | 2870  | AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCT   | 2929  |
|    |       |  |       |
| Db | 71390 | AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCT   | 71331 |
| Qy | 2930  | TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAG  | 2989  |
|    |       |  |       |
| Db | 71330 | TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAG  | 71271 |
| Qy | 2990  | GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT   | 3049  |
|    |       |  |       |
| Db | 71270 | GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT   | 71211 |
| Qy | 3050  | CGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAACACAGTG     | 3109  |
|    |       |  |       |
| Db | 71210 | CGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAACACAGTG     | 71151 |
| Qy | 3110  | CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA  | 3169  |
|    |       |  |       |
| Db | 71150 | CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA  | 71091 |
| Qy | 3170  | AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA   | 3229  |
|    |       |  |       |
| Db | 71090 | AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA   | 71031 |
| Qy | 3230  | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA    | 3289  |
|    |       |  |       |
| Db | 71030 | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA    | 70971 |
| Qy | 3290  | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTACACACCCATATGGATTCTATTT   | 3349  |
|    |       |  |       |
| Db | 70970 | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTACACACCCATATGGATTCTATTT   | 70911 |
| Qy | 3350  | ATAAATCACCCACAACTTGTTCCTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT  | 3409  |
|    |       |  |       |
| Db | 70910 | ATAAATCACCCACAACTTGTTCCTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT  | 70851 |
| Qy | 3410  | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA   | 3469  |
|    |       |  |       |
| Db | 70850 | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA   | 70791 |
| Qy | 3470  | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT   | 3529  |
|    |       |  |       |
| Db | 70790 | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT   | 70731 |

|    |       |  |       |
|----|-------|--|-------|
| Qy | 3530  | GAATTTTACATCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC  | 3589  |
|    |       |  |       |
| Db | 70730 | GAATTTTACATCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC  | 70671 |
| Qy | 3590  | TTGCCAAATTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA  | 3649  |
|    |       |  |       |
| Db | 70670 | TTGCCAAATTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA  | 70611 |
| Qy | 3650  | TTCAGTGGCTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA    | 3709  |
|    |       |  |       |
| Db | 70610 | TTCAGTGGCTTTT-AAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA   | 70552 |
| Qy | 3710  | ACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT  | 3769  |
|    |       |  |       |
| Db | 70551 | ACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT  | 70492 |
| Qy | 3770  | TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTAA  | 3829  |
|    |       |  |       |
| Db | 70491 | TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTAA  | 70432 |
| Qy | 3830  | CATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT  | 3889  |
|    |       |  |       |
| Db | 70431 | CATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT  | 70372 |
| Qy | 3890  | CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC | 3949  |
|    |       |  |       |
| Db | 70371 | CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC | 70312 |
| Qy | 3950  | AAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA   | 4009  |
|    |       |  |       |
| Db | 70311 | AAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA   | 70252 |
| Qy | 4010  | TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA | 4069  |
|    |       |  |       |
| Db | 70251 | TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA | 70192 |
| Qy | 4070  | GTTACTGATTTTTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTA     | 4129  |
|    |       |  |       |
| Db | 70191 | GTTACTGATTTTTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTA     | 70132 |
| Qy | 4130  | CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAA | 4189  |
|    |       |  |       |
| Db | 70131 | CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAA | 70072 |
| Qy | 4190  | TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA | 4249  |
|    |       |  |       |
| Db | 70071 | TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA | 70012 |
| Qy | 4250  | GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG                        | 4286  |
|    |       |  |       |
| Db | 70011 | GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG                        | 69975 |

RESULT 9

US-10-116-802-117

; Sequence 117, Application US/10116802

; Publication No. US20030065157A1

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; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 117
; LENGTH: 1892
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1094000.5
US-10-116-802-117
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Query Match          39.2%; Score 1684.6; DB 13; Length 1892;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1698; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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Qy      178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237
      ||  || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      190 TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 249

Qy      238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      250 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 309

Qy      298 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 357
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      310 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 369

Qy      358 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 417
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      370 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 429

Qy      418 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 477
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      430 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 489

Qy      478 CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 537
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      490 CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 549

Qy      538 AAATACATCAACACGGTTGTGTCTTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC 597
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      550 AAATACATCAACACGGTTGTGTCTTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC 609

Qy      598 ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC 657
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      610 ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC 669

Qy      658 GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC 717
      |||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 670 GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC 729  
 Qy 718 AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA 777  
 |||||  
 Db 730 AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA 789  
 Qy 778 CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT 837  
 |||||  
 Db 790 CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT 849  
 Qy 838 CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA 897  
 |||||  
 Db 850 CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA 909  
 Qy 898 GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCT-GGCTGTCCCTGAAGCCATAGGTTT 956  
 |||||  
 Db 910 GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGGCTGTCCCTGAAGCCATAGGTTT 969  
 Qy 957 TGATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGT 1016  
 |||||  
 Db 970 TGATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGT 1029  
 Qy 1017 TCAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTT 1076  
 |||||  
 Db 1030 TCAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTT 1089  
 Qy 1077 CTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTATACACTAATGACCTGTGAAAT 1136  
 |||||  
 Db 1090 CTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTATACACTAATGACCTGTGAAAT 1149  
 Qy 1137 GTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGA 1196  
 |||||  
 Db 1150 GTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGA 1209  
 Qy 1197 AGTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCA 1256  
 |||||  
 Db 1210 AGTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCA 1269  
 Qy 1257 CCTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACT 1316  
 |||||  
 Db 1270 CCTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACT 1329  
 Qy 1317 TTTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTG 1376  
 |||||  
 Db 1330 TTTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTG 1389  
 Qy 1377 CATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATG 1436  
 |||||  
 Db 1390 CATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATG 1449  
 Qy 1437 CTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTG 1496  
 |||||  
 Db 1450 CTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTG 1509  
 Qy 1497 CTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAG 1556  
 |||||  
 Db 1510 CTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAG 1569

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Qy      1557 CTCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCA 1616
          |||
Db      1570 CTCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCA 1629

Qy      1617 TTAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACA 1676
          |||
Db      1630 TTAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACA 1689

Qy      1677 CTATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAG 1736
          |||
Db      1690 CTATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAG 1749

Qy      1737 CTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACT 1796
          |||
Db      1750 CTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACT 1809

Qy      1797 TAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAA 1856
          |||
Db      1810 TAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAA 1869

Qy      1857 CACTTAGGCTTAAAAATGAGCTC 1879
          |||
Db      1870 CACTTAGGCTTAAAAATGAGCTC 1892

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RESULT 10

US-10-116-802-118

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; Sequence 118, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 1877
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1222734CB1
US-10-116-802-118

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Query Match          39.0%; Score 1676.6; DB 13; Length 1877;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237
          ||
Db      190 TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 249

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|    |      |  |      |
|----|------|--|------|
| Qy | 238  | ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC   | 297  |
|    |      |  |      |
| Db | 250  | ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC   | 309  |
| Qy | 298  | CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG   | 357  |
|    |      |  |      |
| Db | 310  | CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG   | 369  |
| Qy | 358  | CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC   | 417  |
|    |      |  |      |
| Db | 370  | CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC   | 429  |
| Qy | 418  | AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT   | 477  |
|    |      |  |      |
| Db | 430  | AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT   | 489  |
| Qy | 478  | CCGCCACGCACCATCTCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC     | 537  |
|    |      |  |      |
| Db | 490  | CCGCCACGCACCATCTCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC     | 549  |
| Qy | 538  | AAATACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTC   | 597  |
|    |      |  |      |
| Db | 550  | AAATACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTC   | 609  |
| Qy | 598  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 657  |
|    |      |  |      |
| Db | 610  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 669  |
| Qy | 658  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 717  |
|    |      |  |      |
| Db | 670  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 729  |
| Qy | 718  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA  | 777  |
|    |      |  |      |
| Db | 730  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA  | 789  |
| Qy | 778  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 837  |
|    |      |  |      |
| Db | 790  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 849  |
| Qy | 838  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTA    | 897  |
|    |      |  |      |
| Db | 850  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTA    | 909  |
| Qy | 898  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 957  |
|    |      |  |      |
| Db | 910  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 969  |
| Qy | 958  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1017 |
|    |      |  |      |
| Db | 970  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1029 |
| Qy | 1018 | CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC | 1077 |
|    |      |  |      |
| Db | 1030 | CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC | 1089 |
| Qy | 1078 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACATAATGACCTGTGAAATG   | 1137 |

|    |      |   |      |
|----|------|---|------|
| Db | 1090 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTATACACTAATGACCTGTGAAATG     | 1149 |
| Qy | 1138 | TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA | 1197 |
| Db | 1150 | TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA | 1209 |
| Qy | 1198 | GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC  | 1257 |
| Db | 1210 | GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC  | 1269 |
| Qy | 1258 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT  | 1317 |
| Db | 1270 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT  | 1329 |
| Qy | 1318 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC  | 1377 |
| Db | 1330 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC  | 1389 |
| Qy | 1378 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC | 1437 |
| Db | 1390 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC | 1449 |
| Qy | 1438 | TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC  | 1497 |
| Db | 1450 | TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC  | 1509 |
| Qy | 1498 | TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC  | 1557 |
| Db | 1510 | TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC  | 1569 |
| Qy | 1558 | TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT  | 1617 |
| Db | 1570 | TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT  | 1629 |
| Qy | 1618 | TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC  | 1677 |
| Db | 1630 | TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC  | 1689 |
| Qy | 1678 | TATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC   | 1737 |
| Db | 1690 | TATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC   | 1749 |
| Qy | 1738 | TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT  | 1797 |
| Db | 1750 | TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT  | 1809 |
| Qy | 1798 | AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC  | 1857 |
| Db | 1810 | AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC  | 1869 |
| Qy | 1858 | ACT 1860  |      |
| Db | 1870 | ACT 1872  |      |

US-10-305-720-1203  
 ; Sequence 1203, Application US/10305720  
 ; Publication No. US20040010136A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.  
 ; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene  
 Expression  
 ; FILE REFERENCE: PA-0002-1 CON  
 ; CURRENT APPLICATION NUMBER: US/10/305,720  
 ; CURRENT FILING DATE: 2002-11-26  
 ; PRIOR APPLICATION NUMBER: 09/016,434  
 ; PRIOR FILING DATE: 1998-01-30  
 ; NUMBER OF SEQ ID NOS: 1490  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 1203  
 ; LENGTH: 1470  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; OTHER INFORMATION: GenBank ID No. US20040010136A1 gl82275  
 US-10-305-720-1203

Query Match 34.1%; Score 1466.8; DB 16; Length 1470;  
 Best Local Similarity 99.9%; Pred. No. 8.3e-291;  
 Matches 1468; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 192 | GAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC  | 251 |
|    |     |   |     |
| Db | 1   | GAAACTGCGGACGGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC  | 60  |
| Qy | 252 | AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTCGCGGATCTG  | 311 |
|    |     |   |     |
| Db | 61  | AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTCGCGGATCTG  | 120 |
| Qy | 312 | GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGAT  | 371 |
|    |     |   |     |
| Db | 121 | GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGAT  | 180 |
| Qy | 372 | AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC  | 431 |
|    |     |   |     |
| Db | 181 | AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC  | 240 |
| Qy | 432 | GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT  | 491 |
|    |     |   |     |
| Db | 241 | GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT  | 300 |
| Qy | 492 | CTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC | 551 |
|    |     |   |     |
| Db | 301 | CTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC | 360 |
| Qy | 552 | GGTTGTGTCTTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACACTTCTGAGAAT  | 611 |
|    |     |   |     |
| Db | 361 | GGTTGTGTCTTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACACTTCTGAGAAT  | 420 |
| Qy | 612 | TATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCT  | 671 |
|    |     |   |     |



|    |      |   |      |
|----|------|---|------|
| Db | 421  | TATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCT  | 480  |
| Qy | 672  | GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA  | 731  |
|    |      |   |      |
| Db | 481  | GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA  | 540  |
| Qy | 732  | GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGT  | 791  |
|    |      |   |      |
| Db | 541  | GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGT  | 600  |
| Qy | 792  | GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC  | 851  |
|    |      |   |      |
| Db | 601  | GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC  | 660  |
| Qy | 852  | TTGGAGTAGAATTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAAATTGTTTTGAT   | 911  |
|    |      |   |      |
| Db | 661  | TTGGAGTAGAATTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAAATTGTTTTGAT   | 720  |
| Qy | 912  | TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGAT  | 971  |
|    |      |   |      |
| Db | 721  | TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGAT  | 780  |
| Qy | 972  | GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT  | 1031 |
|    |      |   |      |
| Db | 781  | GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT  | 840  |
| Qy | 1032 | CATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTCAGTTTTCTATTTCTGCTTGCC  | 1091 |
|    |      |   |      |
| Db | 841  | CATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTCAGTTTTCTATTTCTGCTTGCC  | 900  |
| Qy | 1092 | ATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAG | 1151 |
|    |      |   |      |
| Db | 901  | ATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAG | 960  |
| Qy | 1152 | TGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGT  | 1211 |
|    |      |   |      |
| Db | 961  | TGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGT  | 1020 |
| Qy | 1212 | CTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCT   | 1271 |
|    |      |   |      |
| Db | 1021 | CTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCT   | 1080 |
| Qy | 1272 | GAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTTTCTGTT | 1331 |
|    |      |   |      |
| Db | 1081 | GAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTTTCTGTT | 1140 |
| Qy | 1332 | GGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGC  | 1391 |
|    |      |   |      |
| Db | 1141 | GGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGC  | 1200 |
| Qy | 1392 | TCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTG   | 1451 |
|    |      |   |      |
| Db | 1201 | TCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTG   | 1260 |
| Qy | 1452 | CCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGC  | 1511 |
|    |      |   |      |
| Db | 1261 | CCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGC  | 1320 |

Qy 1512 TAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAA 1571  
 |||  
 Db 1321 TAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAA 1380  
 Qy 1572 GAACTATTCACTGTATTTTCAATTTTCTTTATATTGGACCGAAGTCATTAAAAACAAAATGAA 1631  
 |||  
 Db 1381 GAACTATTCACTGTATTTTCAATTTTCTTTATATTGGACCGAAGTCATTAAAAACAAAATGAA 1440  
 Qy 1632 ACATTTGCCAAAACAAAACAAAAAACTATG 1661  
 |||  
 Db 1441 ACATTTGCCAAAACAAAACAAAAAACTATG 1470

RESULT 12

US-10-311-671-28

; Sequence 28, Application US/10311671

; Publication No. US20040072996A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: LAL, Preeti G.

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: HAFALIA, April J. A.

; APPLICANT: NGUYEN, Danniel B.

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: KALLICK, Deborah A.

; APPLICANT: GRIFFIN, Jennifer A.

; APPLICANT: YUE, Henry

; APPLICANT: KHAN, Farrah A.

; APPLICANT: ARVIZU, Chandra S.

; APPLICANT: LU, Dyung Aina M.

; APPLICANT: TRIBOULEY, Catherine M.

; APPLICANT: LU, Yan

; APPLICANT: CHAWLA, Narinder K.

; APPLICANT: GRAUL, Richard

; APPLICANT: YAO, Monique G.

; APPLICANT: YANG, Junming

; APPLICANT: RAMKUMAR, Jayalaxmi

; APPLICANT: AU-YOUNG, Janice K.

; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: HERNANDEZ, Roberto

; APPLICANT: WALSH, Roderick T.

; APPLICANT: BOROWSKY, Mark L.

; APPLICANT: THORNTON, Michael B.

; APPLICANT: HE, Ann

; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS

; FILE REFERENCE: PI-0131 USN

; CURRENT APPLICATION NUMBER: US/10/311,671

; CURRENT FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: PCT/US01/19275

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,483

; PRIOR FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: 60/213,954

; PRIOR FILING DATE: 2000-06-22

; PRIOR APPLICATION NUMBER: 60/215,209

; PRIOR FILING DATE: 2000-06-29

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; PRIOR APPLICATION NUMBER: 60/216,595
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,936
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/219,154
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/220,141
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 1632
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 6792419CB1
US-10-311-671-28

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Query Match          32.3%; Score 1389; DB 12; Length 1632;
Best Local Similarity 100.0%; Pred. No. 8.6e-275;
Matches 1389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      186 GGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCC 245
          |||
Db      236 GGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCC 295

Qy      246 GCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTCGCG 305
          |||
Db      296 GCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTCGCG 355

Qy      306 GATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGC 365
          |||
Db      356 GATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGC 415

Qy      366 AGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGC 425
          |||
Db      416 AGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGC 475

Qy      426 GCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACG 485
          |||
Db      476 GCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACG 535

Qy      486 CACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACAT 545
          |||
Db      536 CACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACAT 595

Qy      546 CAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCT 605
          |||
Db      596 CAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCT 655

Qy      606 GAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTT 665
          |||
Db      656 GAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTT 715

Qy      666 GGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCT 725
          |||

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|    |      |   |      |
|----|------|---|------|
| Db | 716  | GGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCT  | 775  |
| Qy | 726  | GGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGC  | 785  |
|    |      |   |      |
| Db | 776  | GGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGC  | 835  |
| Qy | 786  | CTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGT  | 845  |
|    |      |   |      |
| Db | 836  | CTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGT  | 895  |
| Qy | 846  | TGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGT  | 905  |
|    |      |   |      |
| Db | 896  | TGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGT  | 955  |
| Qy | 906  | TTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTGTATATAAT  | 965  |
|    |      |   |      |
| Db | 956  | TTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTGTATATAAT  | 1015 |
| Qy | 966  | TACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGAC  | 1025 |
|    |      |   |      |
| Db | 1016 | TACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGAC  | 1075 |
| Qy | 1026 | AGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTG | 1085 |
|    |      |   |      |
| Db | 1076 | AGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTG | 1135 |
| Qy | 1086 | CTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAA  | 1145 |
|    |      |   |      |
| Db | 1136 | CTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAA  | 1195 |
| Qy | 1146 | GAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAA  | 1205 |
|    |      |   |      |
| Db | 1196 | GAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAA  | 1255 |
| Qy | 1206 | AACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCCTTCACCTCAGCAG | 1265 |
|    |      |   |      |
| Db | 1256 | AACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCCTTCACCTCAGCAG | 1315 |
| Qy | 1266 | GATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTT | 1325 |
|    |      |   |      |
| Db | 1316 | GATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTT | 1375 |
| Qy | 1326 | TCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCC  | 1385 |
|    |      |   |      |
| Db | 1376 | TCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCC  | 1435 |
| Qy | 1386 | AATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTG | 1445 |
|    |      |   |      |
| Db | 1436 | AATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTG | 1495 |
| Qy | 1446 | CTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTT  | 1505 |
|    |      |   |      |
| Db | 1496 | CTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTT  | 1555 |
| Qy | 1506 | CAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTG  | 1565 |
|    |      |   |      |
| Db | 1556 | CAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTG  | 1615 |

Qy 1566 AAAGAAGAA 1574  
|||||||  
Db 1616 AAAGAAGAA 1624

RESULT 13

US-09-826-509-496

; Sequence 496, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated  
Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 496

; LENGTH: 1329

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-826-509-496

Query Match 30.8%; Score 1322.6; DB 11; Length 1329;

Best Local Similarity 99.7%; Pred. No. 3.3e-261;

Matches 1325; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297  
|||||||  
Db 1 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 60

Qy 298 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 357  
|||||||  
Db 61 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCGACAGGGCCACTCCGCTTTTG 120

Qy 358 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 417  
|||||||  
Db 121 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 180

Qy 418 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 477  
|||||||  
Db 181 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 240

Qy 478 CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 537  
|||||||  
Db 241 CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 300

Qy 538 AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC 597

|    |      |  |      |
|----|------|--|------|
| Db | 301  | <br>AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC | 360  |
| Qy | 598  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC       | 657  |
| Db | 361  | <br>ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 420  |
| Qy | 658  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC       | 717  |
| Db | 421  | <br>GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 480  |
| Qy | 718  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA       | 777  |
| Db | 481  | <br>AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA   | 540  |
| Qy | 778  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT       | 837  |
| Db | 541  | <br>CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 600  |
| Qy | 838  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTCCAAAATGGACAGCAGTA         | 897  |
| Db | 601  | <br>CGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTCCAAAATGGACAGCAGTA     | 660  |
| Qy | 898  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT       | 957  |
| Db | 661  | <br>GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 720  |
| Qy | 958  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT       | 1017 |
| Db | 721  | <br>GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 780  |
| Qy | 1018 | CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC      | 1077 |
| Db | 781  | <br>CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC  | 840  |
| Qy | 1078 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG      | 1137 |
| Db | 841  | <br>TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG  | 900  |
| Qy | 1138 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA       | 1197 |
| Db | 901  | <br>TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA   | 960  |
| Qy | 1198 | GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC       | 1257 |
| Db | 961  | <br>GTGAAGAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC   | 1020 |
| Qy | 1258 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT       | 1317 |
| Db | 1021 | <br>CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT   | 1080 |
| Qy | 1318 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC       | 1377 |
| Db | 1081 | <br>TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC   | 1140 |
| Qy | 1378 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGC        | 1437 |
|    |      |  |      |

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Db      1141 ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC 1200
Qy      1438 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC 1497
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC 1260
Qy      1498 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC 1557
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC 1320
Qy      1558 TCATCTTGA 1566
        ||||||||
Db      1321 TCATCTTGA 1329

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RESULT 14

US-10-235-192A-32

; Sequence 32, Application US/10235192A

; Publication No. US20040043389A1

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Jeanette

; TITLE OF INVENTION: Methods and Compositions for Identifying

; TITLE OF INVENTION: Risk Factors for Abnormal Lipid Levels and the Diseases

; TITLE OF INVENTION: and Disorders Associated Therewith

; FILE REFERENCE: MMI-011

; CURRENT APPLICATION NUMBER: US/10/235,192A

; CURRENT FILING DATE: 2002-09-04

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 32

; LENGTH: 1578

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-235-192A-32

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Query Match          28.4%; Score 1220.4; DB 13; Length 1578;
Best Local Similarity 99.8%; Pred. No. 3.6e-240;
Matches 1228; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy      203 GCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCCAAGTCTGTGCG 262
        ||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db      200 GCGGCCACCGGACG-CTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCCAAGTCTGTGCG 258
Qy      263 GACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTCGCGGATCTGGGGAGAGGAGA 322
        ||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db      259 GACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTCGCGGATCTGGGGAGAGGAGA 318
Qy      323 GAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCCAC 382
        ||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db      319 GAGGCTTCCCGCCCACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCCAC 378
Qy      383 CCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGGGTCTGTTGGCACCTG 442
        ||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db      379 CCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGGGTCTGTTGGCACCTG 438
Qy      443 CGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCCCC 502
        ||||||||||||| |||||||||||||||||||||||||||||||||||||||

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|    |      |  |      |
|----|------|--|------|
| Db | 439  | CGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCCCC   | 498  |
| Qy | 503  | CGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCT   | 562  |
| Db | 499  | CGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCT   | 558  |
| Qy | 563  | GCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGA | 622  |
| Db | 559  | GCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGA | 618  |
| Qy | 623  | ACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGC   | 682  |
| Db | 619  | ACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGC   | 678  |
| Qy | 683  | TGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCAT   | 742  |
| Db | 679  | TGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCAT   | 738  |
| Qy | 743  | TTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTG   | 802  |
| Db | 739  | TTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTG   | 798  |
| Qy | 803  | TGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAA   | 862  |
| Db | 799  | TGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAA   | 858  |
| Qy | 863  | TTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTGTATTTGGGTGGTCT   | 922  |
| Db | 859  | TTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTGTATTTGGGTGGTCT   | 918  |
| Qy | 923  | CTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAG   | 982  |
| Db | 919  | CTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAG   | 978  |
| Qy | 983  | GAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGTTTT   | 1042 |
| Db | 979  | GAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGTTTT   | 1038 |
| Qy | 1043 | ACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCA  | 1102 |
| Db | 1039 | ACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCA  | 1098 |
| Qy | 1103 | CTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAAGAAAAGTGGCATGCAGA | 1162 |
| Db | 1099 | CTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAAGAAAAGTGGCATGCAGA | 1158 |
| Qy | 1163 | TTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGG   | 1222 |
| Db | 1159 | TTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGG   | 1218 |
| Qy | 1223 | TCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTC   | 1282 |
| Db | 1219 | TCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTC   | 1278 |
| Qy | 1283 | TTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACT   | 1342 |
| Db | 1279 | TTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACT   | 1338 |



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Qy      1343 ATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGG 1402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1339 ATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGG 1398

Qy      1403 TGAGCAAAGATTCAAAAAGTCTTTAAGTC 1433
          ||||||||||||||||||||
Db      1399 TGAGCAAAGATTCAAAAAGTCTTTAAGGC 1429

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RESULT 15

US-09-778-927A-27

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; Sequence 27, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL 134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 800
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(800 )
; OTHER INFORMATION: n = a,c,g,t any unknown or other
US-09-778-927A-27

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Query Match          17.7%; Score 763.2; DB 9; Length 800;
Best Local Similarity 98.3%; Pred. No. 2e-146;
Matches 771; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy      61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy      121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy      181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

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|    |     |  |     |
|----|-----|--|-----|
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG | 300 |
|    |     |  |     |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA | 360 |
|    |     |  |     |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT | 420 |
|    |     |  |     |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT | 420 |
| Qy | 421 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
|    |     |  |     |
| Db | 421 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |
|    |     |  |     |
| Db | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |
| Qy | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAC      | 600 |
|    |     |  |     |
| Db | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAC      | 600 |
| Qy | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC | 660 |
|    |     |  |     |
| Db | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC | 660 |
| Qy | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG | 720 |
|    |     |  |     |
| Db | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG | 720 |
| Qy | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG | 780 |
|    |     |  |     |
| Db | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGCCAGGTAGGAGCGTTCACCCAC | 780 |
| Qy | 781 | AAAG   | 784 |
|    |     |  |     |
| Db | 781 | CCAG   | 784 |

Search completed: May 15, 2004, 00:12:39  
 Job time : 1645.24 secs